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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:51 ; Search time 56 Seconds

(without alignments)
1635.451 Million cell updates/sec

Title: US-09-915-515a-1

Perfect score: 2998
Sequence: 1 MDRVSGVALENDERAKNT.....IVPLVEILKNDGVREARSG 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2998	100.0	577	23 AA014442	Protein of Newcastle
2	2993	99.8	577	18 AA018228	Paramyxovirus haem
3	2985	99.6	577	4 AAP70843	Sequence of Newcas
4	2920	97.4	577	14 AAR39703	Haemagglutinin-neu
5	2920	97.4	577	15 AAR80558	Newcastle's disease
6	2920	97.4	577	17 AAR05827	Newcastle disease
7	2920	97.4	577	21 AAY51232	Newcastle disease
8	2915	97.2	581	15 AAR58559	Newcastle disease
9	2915	97.2	581	15 AAR58559	Newcastle disease

10	2915	97.2	581	18 AAM10690	Newcastle disease
11	2915	97.2	581	20 AAY21982	Seq ID No: 13 of U
12	2915	97.2	581	21 AAB36038	Protein encoded by
13	2915	97.2	581	21 AAY58182	NDV haemagglutinin
14	2847	95.0	616	10 AAP6147	Sequence of Newcas
15	2839	94.7	616	11 AAR06329	Newcastle disease
16	2742	91.5	571	19 AAM44940	Newcastle disease
17	2735	91.2	568	19 AAM62989	HN protein of Newc
18	2727	91.0	568	17 AAM03551	Newcastle disease
19	2727	91.0	568	17 AAM03138	Newcastle disease
20	2727	91.0	568	17 AAM03325	Newcastle disease
21	2727	91.0	568	19 AAM49683	Newcastle disease
22	2679	89.4	571	10 AAP91960	Haemagglutinin and
23	2390	79.7	453	10 AAP81829	Paramyxovirus solu
24	776	25.9	565	24 ABJ18511	Human Cryptovirus
25	773	25.8	582	22 AAB67478	Amino acid sequenc
26	770	25.7	582	22 AAB93666	Haemagglutinin-neu
27	479	16.0	575	23 AAU79234	Sendai virus HN (h
28	449	15.0	572	10 AAP94799	Perdue strain of t
29	449	15.0	572	10 AAP94800	Parainfluenzae-3 g
30	449	15.0	572	14 AAR31957	Sequence encoded b
31	449	15.0	572	16 AAR79037	PI-3 haemagglutini
32	444.5	14.8	572	21 AAB08627	Amino acid sequenc
33	442.5	14.8	572	14 AAR39284	Parainfluenza viru
34	441.5	14.7	572	23 AAU74678	Parainfluenza viru
35	428.5	14.3	572	11 AAR06023	Viral haemagglutin
36	395.5	13.2	558	6 AAP50501	Sequence of bovine
37	205	6.8	36	20 AAB75537	Antigenic site of
38	184	6.1	33	20 AAB75507	Antigenic site of
39	145	4.8	1723	23 AAB94267	Chlamydia pneumoni
40	144	4.8	1723	23 AAB90585	Chlamydia pneumoni
41	144	4.8	1723	23 AAB94266	Chlamydia pneumoni
42	122	4.1	22	20 AAB97457	Antigenic site of
43	119	4.0	881	22 AAG70752	S cerevisiae apopt
44	119	4.0	1198	20 AAT92428	Amino acid sequenc
45	116	3.9	2261	24 ABJ18914	Pathogen specific

ALIGNMENTS

RESULT 1	
AA014442	
ID	AA014442 standard; protein: 577 AA.
XX	XX
AC	AA014442;
XX	XX
DT	09-MAY-2002 (first entry)
XX	XX
DE	Protein of Newcastle Disease Virus Haemagglutinin-Neuraminidase.
XX	XX
KW	Paramyxovirus haemagglutinin-neuraminidase; HN; x-ray crystallography;
KW	crystal form; inhibitor; antiinflammatory; virucide; infection; croup;
KW	bronchitis; pneumonia; respiratory disease; Newcastle disease virus; NDV.
XX	XX
OS	Newcastle disease virus.
XX	XX
PN	MO200210459-A2.
XX	XX
PD	07-FEB-2002.
XX	XX
PF	27-JUL-2001; 2001WO-US23623.
XX	XX
PR	27-JUL-2000; 2000US-221199P.
XX	XX
PA	(BIOC-) BIOCRYST PHARM INC.
PA	(STUD-) ST JUDS CHILDREN'S RES HOSPITAL.
PA	(UYSA-) UNIV ST ANDREWS.
PA	(UYBA-) UNIV BATH.
XX	XX
PI	Taylor G, Portner A, Takamoto T, Babu VS, Rowland RS;
XX	DR
WPI	2002-195970/25.

XX Identifying paramyxovirus haemagglutinin neuraminidase (HN) inhibitor
 PT useful for treating or preventing group, by applying three-dimensional
 PT structure of active site of paramyxovirus HN to design or select
 PT inhibitor

XX Claim 1; Page 30; 30pp; English.

XX The invention relates to structures of paramyxovirus haemagglutinin-
 CC neuraminidases (HN), as determined by x-ray crystallography, the use of
 CC such structures to solve the structure of paramyxovirus HN homologues,
 CC mutants, co-complexes, and other crystal forms and the use of such
 CC structures, their homologues, mutants, co-complexes, and other crystal
 CC forms, to design inhibitors of paramyxovirus HN. The paramyxovirus HN's
 CC have anti-inflammatory and virucide activity and can be used for
 CC identifying a potential inhibitor of paramyxovirus HN. The paramyxovirus
 CC HN of the invention useful for treating or preventing undesired
 CC properties of infection by paramyxoviruses, and thus for treating or
 CC preventing group, bronchitis, pneumonia, or any other respiratory disease
 CC caused by paramyxovirus. This sequence represents the protein of
 CC Newcastle Disease Virus (NDV) Haemagglutinin-Neuraminidase of the
 CC invention.

XX Sequence 577 AA;

Query Match 100.0%; Score 2998; DB 23; Length 577;

Best Local Similarity 100.0%; Pred. No. 5.5e-283;

Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRASQVLENDERAKNTWRLIFRIAILLTVTTLATSVASLVSMGASPSDLVGIP 60
 DB 1 MDRASQVLENDERAKNTWRLIFRIAILLTVTTLATSVASLVSMGASPSDLVGIP 60
 QY 61 TRISRAEKITSLGSDVVDRIYQVLESPLALNTETIMNATSLSYQINGAANN 120
 DB 61 TRISRAEKITSLGSDVVDRIYQVLESPLALNTETIMNATSLSYQINGAANN 120
 QY 121 SGWGAPIHDDPFIIGIGIKELIVDNASDVTSFYPSAQEHINFIAPATTSGGCTRIIPSDM 180
 DB 121 SGWGAPIHDDPFIIGIGIKELIVDNASDVTSFYPSAQEHINFIAPATTSGGCTRIIPSDM 180
 QY 181 SATHYCYTHNVLLSGCRDHS HQYALGVLTATGRIFPSTLRISLDDTONRSCSV 240
 DB 181 SATHYCYTHNVLLSGCRDHS HQYALGVLTATGRIFPSTLRISLDDTONRSCSV 240
 QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDQYHEKODLVTTLPEDWVANY 300
 DB 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDQYHEKODLVTTLPEDWVANY 300
 QY 301 GVGGSFIDGRVWPSVYGGKPNSSPDTVOEGKVIYKRYNDTCPPDEODYQIMAKSSYK 360
 DB 301 GVGGSFIDGRVWPSVYGGKPNSSPDTVOEGKVIYKRYNDTCPPDEODYQIMAKSSYK 360
 QY 361 GGRFGKRIQOAILISIKVSTSLGEPVLTVPNTVTLMAGEGRILTVGTSHFLYQGRSSY 420
 DB 361 GGRFGKRIQOAILISIKVSTSLGEPVLTVPNTVTLMAGEGRILTVGTSHFLYQGRSSY 420
 QY 421 FSPALLYPMVVSNTKATLHSPYTFNATPRGSIIPCOASARCSPNSCVGVTTDPPLFYR 480
 DB 421 FSPALLYPMVVSNTKATLHSPYTFNATPRGSIIPCOASARCSPNSCVGVTTDPPLFYR 480
 QY 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRTTRYSSTKAAVYTSCTCFKVKTKNTK 540
 DB 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRTTRYSSTKAAVYTSCTCFKVKTKNTK 540
 QY 541 YCLSIASISNTLFGREFRIVPLVLEILKNDGVREARSG 577
 DB 541 YCLSIASISNTLFGREFRIVPLVLEILKNDGVREARSG 577

RESULT 2
 AAM18228
 ID AAM18228 standard; Protein; 577 AA.

XX AC AAM18228;
 XX 24-SEP-1997 (first entry)
 DT
 XX Paramyxovirus haemagglutinin neuraminidase.
 DE
 XX Viral attachment protein; virosome; haemagglutinin neuraminidase;
 KM paramyxovirus; crystallisation.
 OS
 XX Newcastle disease virus Kansas strain.

XX Key Location/Qualifiers
 FT Cleavage-site 124..125
 FT Protein 126..557
 FT /note="soluble VAP"

XX MO9709345-A1.

XX 13-MAR-1997.

XX 06-SEP-1996; 96WO-US14187.

XX 08-SEP-1995; 95US-0003447.

XX (SJD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Portner A, Takimoto T;

XX MPI; 1997-192839/17.

XX N-PSDB; AAT71745.

PT Crystallisation of viral attachment protein - by cleaving the
 PT protein from a virosome and producing crystals by hanging drop
 PT vapour diffusion

PS Claim 14; Page 30; 41pp; English.

XX Haemagglutinin neuraminidase (HN) (AAM18228) is a viral attachment
 CC protein (VAP) of Newcastle disease virus (NDV). Its amino acid
 CC sequence was deduced from a gene (AAT71747) derived from virus-
 CC infected BHK cells. A method of crystallising a VAP such as HN
 CC involves: providing a purified virosome derived from a virus
 CC contg. the VAP in membrane-bound form; proteolytic cleavage of
 CC the VAP to provide a soluble form (see also AAM18229) of the VAP;
 CC and crystallising the cleaved VAP using a hanging drop vapour
 CC diffusion method. The crystallised VAP can be used to provide
 CC a 3-dimensional structure for use in the rational design of
 CC inhibitors to treat viral infections.

XX Sequence 577 AA;

Query Match 99.8%; Score 2993; DB 18; Length 577;

Best Local Similarity 99.7%; Pred. No. 1.7e-282;

Matches 575; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDRASQVLENDERAKNTWRLIFRIAILLTVTTLATSVASLVSMGASPSDLVGIP 60
 DB 1 MDRASQVLENDERAKNTWRLIFRIAILLTVTTLATSVASLVSMGASPSDLVGIP 60
 QY 61 TRISRAEKITSLGSDVVDRIYQVLESPLALNTETIMNATSLSYQINGAANN 120
 DB 61 TRISRAEKITSLGSDVVDRIYQVLESPLALNTETIMNATSLSYQINGAANN 120
 QY 121 SGWGAPIHDDPFIIGIGIKELIVDNASDVTSFYPSAQEHINFIAPATTSGGCTRIIPSDM 180
 DB 121 SGWGAPIHDDPFIIGIGIKELIVDNASDVTSFYPSAQEHINFIAPATTSGGCTRIIPSDM 180
 QY 181 SATHYCYTHNVLLSGCRDHS HQYALGVLTATGRIFPSTLRISLDDTONRSCSV 240
 DB 181 SATHYCYTHNVLLSGCRDHS HQYALGVLTATGRIFPSTLRISLDDTONRSCSV 240
 QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDQYHEKODLVTTLPEDWVANY 300

QY 241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGRIGFGQIHEKDLDTTLFEDWVANYP 300
 DB 241 SATPLGCDMLCSKATETEBEDYNSAVPTLMAHGRIGFGQIHEKDLDTTLFEDWVANYP 300
 QY 301 GVGGSFIDGRVWFSVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360
 DB 301 GVGGSFIDGRVWFSVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360
 QY 361 GFRFGKRIQOALISIKVSTSLGSDPVLTPPNTVTLMAEGRILTVGSHFLYORGSSY 420
 DB 361 GFRFGKRIQOALISIKVSTSLGSDPVLTPPNTVTLMAEGRILTVGSHFLYORGSSY 420
 QY 421 FSPALLYPMYVSNKTATLHSPYTFNAFTPPGSI PCQASARCPNSCVTVGYTDPYPLIFR 480
 DB 421 FSPALLYPMYVSNKTATLHSPYTFNAFTPPGSI PCQASARCPNSCVTVGYTDPYPLIFR 480
 QY 481 NHTLRGVGTMLDSEQARLNPASAVFDSRSRITRVSSSSTKAAYTTSTGKVKTKTKT 540
 DB 481 NHTLRGVGTMLDSEQARLNPASAVFDSRSRITRVSSSSTKAAYTTSTGKVKTKTKT 540
 QY 541 YCLSLAEISNTLFGFPRIVPLVEILKNDGVREARSG 577
 DB 541 YCLSLAEISNTLFGFPRIVPLVEILKNDGVREARSG 577

RESULT 6

AAW06827 standard; Protein; 577 AA.

AAW06827;

03-MAR-1997 (first entry)

Newcastle disease virus haemagglutinin.

Turkey herpes virus; recombinant virus; vaccine; prophylaxis;

immunisation; avian virus; infectious bronchitis virus;

infectious bursal disease virus; Newcastle disease virus;

Marek's disease virus; infectious laryngotracheitis virus; IBV;

IBV; NDV; MDV; ILV.

Newcastle disease virus.

WO9605291-A1.

22-FEB-1996.

09-AUG-1995; 95WO-US10245.

22-DEC-1994; 94US-0362240.

09-AUG-1994; 94US-0288065.

(SYTR) SYNTRO CORP.

Cochran MD, Junker DE, Singer PA, Wild MA;

WPI, 1996-139689/14.

N-PSDB; AAT16205.

Recombinant turkey herpes viruses contg. foreign DNA encoding a

cytokine - useful in vaccines to protect against Marek's disease

virus and other avian viruses.

Disclosure: Page 175-176; 249pp; English.

Recombinant turkey herpes virus (rTH) which comprise a foreign DNA

sequence encoding a cytokine inserted into a XhoI site within an

ECOR1 #9 genomic fragment, where the cytokine can be expressed in

host cells infected with the virus can be used in vaccines to

protect turkeys against avian viruses. The recombinant viruses can

be used for immunising birds against infectious bronchitis virus

(IBV), infectious bursal disease virus (IBDV), Marek's disease virus

(MDV) infectious laryngotracheitis virus (ILT) and Newcastle disease

virus (NDV). They may also be used in multivalent vaccines to

protect against two or more of these avian viruses. This sequence

is the haemagglutinin protein of the Newcastle disease virus, an

antigen which can be used in the recombinant vaccines.

CC virus (NDV). They may also be used in multivalent vaccines to

protect against two or more of these avian viruses. This sequence

is the haemagglutinin protein of the Newcastle disease virus, an

antigen which can be used in the recombinant vaccines.

Sequence 577 AA;

Query Match 97.4%; Score 2920; DB 17; Length 577;

Best Local Similarity 96.9%; Pred. No. 2.2e-275;

Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRAVSQVLENDEREAKNTWRLIFRIAILLTVTLATSVASLVSKASTPSDLVGP 60
 DB 1 MDRAVSQVLENDEREAKNTWRLIFRIAILLTVTLATSVASLVSKASTPSDLVGP 60
 QY 61 TRISRAEKITSAIGSNODVDVRIYKQVALESPLALNTETTINATSLSYQINGANN 120
 DB 61 TRISRAEKITSAIGSNODVDVRIYKQVALESPLALNTETTINATSLSYQINGANN 120
 QY 121 SGMGAPIHDPDPIGIGIKELIVDNASDVSFPYAPQEHNFIPAPTTGSGCTRIIPSPDM 180
 DB 121 SGMGAPIHDPDPIGIGIKELIVDNASDVSFPYAPQEHNFIPAPTTGSGCTRIIPSPDM 180
 QY 181 SATHYCYTHNVILSGCDHSHSHQYALGVLRRTATGRIFFTLSRISLDDTONRKSQSV 240
 DB 181 SATHYCYTHNVILSGCDHSHSHQYALGVLRRTATGRIFFTLSRISLDDTONRKSQSV 240
 QY 241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGRIGFGQIHEKDLDTTLFEDWVANYP 300
 DB 241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGRIGFGQIHEKDLDTTLFEDWVANYP 300
 QY 301 GVGGSFIDGRVWFSVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360
 DB 301 GVGGSFIDGRVWFSVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360
 QY 361 GFRFGKRIQOALISIKVSTSLGSDPVLTPPNTVTLMAEGRILTVGSHFLYORGSSY 420
 DB 361 GFRFGKRIQOALISIKVSTSLGSDPVLTPPNTVTLMAEGRILTVGSHFLYORGSSY 420
 QY 421 FSPALLYPMYVSNKTATLHSPYTFNAFTPPGSI PCQASARCPNSCVTVGYTDPYPLIFR 480
 DB 421 FSPALLYPMYVSNKTATLHSPYTFNAFTPPGSI PCQASARCPNSCVTVGYTDPYPLIFR 480
 QY 481 NHTLRGVGTMLDSEQARLNPASAVFDSRSRITRVSSSSTKAAYTTSTGKVKTKTKT 540
 DB 481 NHTLRGVGTMLDSEQARLNPASAVFDSRSRITRVSSSSTKAAYTTSTGKVKTKTKT 540
 QY 541 YCLSLAEISNTLFGFPRIVPLVEILKNDGVREARSG 577
 DB 541 YCLSLAEISNTLFGFPRIVPLVEILKNDGVREARSG 577

RESULT 7

AAVS1232 standard; Protein; 577 AA.

AAVS1232;

07-APR-2000 (first entry)

Newcastle disease virus LaSota genome encoded protein 5.

Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;

respiratory disease; gastrointestinal disease; poultry pathogen;

local immunity.

Newcastle disease virus.

WO9966045-A1.

23-DEC-1999.

17-JUN-1999; 99WO-NL00377.

Db 66 RISRAEKITSTLGSNDVDRIRYKQVALBESPLALNTETIMMAITSLSQINGAANS 125
 Qy 122 GMAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPSPDMS 181
 Db 126 GMAPIHDPDVIIGIGIKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPSPDMS 185
 Qy 182 ATHYCYTHNVILSGCRHSHSHQYIALGVLTATGRIFFSTLRSISLDDTQNRKSCSVS 241
 Db 186 ATHYCYTHNVILSGCRHSHSHQYIALGVLTATGRIFFSTLRSISLDDTQNRKSCSVS 245
 Qy 242 ATPGCDMLCSKYTEBEDYNSAVPTLMAGRLGFGDQYHEKOLDVTTLPEDVWVANYPG 301
 Db 246 ATPGCDMLCSKATEBEDYNSAVPTLMAGRLGFGDQYHEKOLDVTTLPEDVWVANYPG 305
 Qy 302 VGGGSFIDGRWFSVYGLKPNPSDVTQEGKYVIYKRYNDTCPEODYOIRMAKSSYKP 361
 Db 306 VGGGSFIDSRWFSVYGLKPNPSDVTQEGKYVIYKRYNDTCPEODYOIRMAKSSYKP 365
 Qy 362 GRFGGKRIQOAILSIKYSTLSGEDPVLTPPNTVTLMGAEGRILTVGTSHEFLYORGSSYF 421
 Db 366 GRFGGKRIQOAILSIKYSTLSGEDPVLTPPNTVTLMGAEGRILTVGTSHEFLYORGSSYF 425
 Qy 422 SPALLYPMTVSNKATLHSPYTFNAFTRPGSIPQASARCPNSCVTVGYTDPYPLIFRYN 481
 Db 426 SPALLYPMTVSNKATLHSPYTFNAFTRPGSIPQASARCPNSCVTVGYTDPYPLIFRYN 485
 Qy 482 HTLRGVFGTMDSEQARLNPASAVFDSTSRIRTRVSSSTKAAYTTSTCFKVVTKNTKY 541
 Db 486 HTLRGVFGTMDSEQARLNPASAVFDSTSRIRTRVSSSTKAAYTTSTCFKVVTKNTKY 545
 Qy 542 CLSTIAEISNTLFGFERRIVPLVEILKNDGVREARSG 577
 Db 546 CLSTIAEISNTLFGFERRIVPLVEILKNDGVREARSG 581

RESULT 9

AARS598
 ID AARS598 standard; Protein; 581 AA.

AC AARS598;
 XX
 DT 25-MAR-2003 (updated)
 DT 14-APR-1995 (first entry)
 XX
 DE Newcastle disease virus HN gene product.
 XX
 KM Newcastle disease virus; HN gene; SfiI; vector 502-26.22.
 XX
 OS Synthetic.
 XX
 PN MO9415015-A1.
 XX
 XX 01-SEP-1994.
 PD
 XX 28-FEB-1994; 94MO-US02252.
 PF
 XX 26-FEB-1993; 93US-0024156.
 PR
 XX (SYTR) SYNTRO CORP.
 PA
 XX Cochran MD;
 PI
 XX MPI: 1994-294008/36.
 DR N-PSDB; AA070570.
 XX
 XX New recombinant fowl pox viruses - useful as vaccines against
 FT fowl pox virus, Newcastle Disease Virus and infectious
 PT laryngotracheitis virus.
 XX
 PS Disclosure; Page 77-79; 97pp; English.
 XX
 CC AA070570 is the SfiI fragment insert in Homology Vector 502-26.22
 CC contg. Newcastle disease virus (NDV) HN and F genes. The structure

CC of the fragment is: 5'- Junction A - Fragment 1 (NDV HN Aas 2-577)
 CC - Junction B - Fragment 2 (NDV F Aas 1-553) - Junction C - Fragment
 CC 3 (PBR322) - Junction D - 3'. Fragment 1 is Avail to NaeI fragment
 CC of the full length NDV HN cDNA clone (B1 strain). Fragment 2 is
 CC BamHI to PstI fragment of the full length NDV F cDNA (B1 strain).
 CC Fragment 3 is a PstI and ScaI fragment of PBR322. The structures
 CC of the Junctions A, B, C and D are given in AA070552, AA070553,
 CC AA070554 and AA070555 respectively.
 CC (updated on 25-MAR-2003 to correct PN field.)

Sequence 581 AA;

Query Match 97.2%; Score 2915; DB 15; Length 581;
 Best Local Similarity 96.9%; Pred. No. 7e-275;
 Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 DRANSQVALNDEBEAKOTWRLIFRIMILLITVTLATSVASLVYSGASTPSDLVGIPT 61
 Db 6 DRAVSQVALNDEBEAKOTWRLIFRIMILLITVTLATSVASLVYSGASTPSDLVGIPT 65
 Qy 62 RISRAEKITSAAGSNDVDRIRYKQVALBESPLALNTETIMMAITSLSQINGAANS 121
 Db 66 RISRAEKITSTLGSNDVDRIRYKQVALBESPLALNTETIMMAITSLSQINGAANS 125
 Qy 122 GMAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPSPDMS 181
 Db 126 GMAPIHDPDVIIGIGIKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPSPDMS 185
 Qy 182 ATHYCYTHNVILSGCRHSHSHQYIALGVLTATGRIFFSTLRSISLDDTQNRKSCSVS 241
 Db 186 ATHYCYTHNVILSGCRHSHSHQYIALGVLTATGRIFFSTLRSISLDDTQNRKSCSVS 245
 Qy 242 ATPGCDMLCSKYTEBEDYNSAVPTLMAGRLGFGDQYHEKOLDVTTLPEDVWVANYPG 301
 Db 246 ATPGCDMLCSKATEBEDYNSAVPTLMAGRLGFGDQYHEKOLDVTTLPEDVWVANYPG 305
 Qy 302 VGGGSFIDGRWFSVYGLKPNPSDVTQEGKYVIYKRYNDTCPEODYOIRMAKSSYKP 361
 Db 306 VGGGSFIDSRWFSVYGLKPNPSDVTQEGKYVIYKRYNDTCPEODYOIRMAKSSYKP 365
 Qy 362 GRFGGKRIQOAILSIKYSTLSGEDPVLTPPNTVTLMGAEGRILTVGTSHEFLYORGSSYF 421
 Db 366 GRFGGKRIQOAILSIKYSTLSGEDPVLTPPNTVTLMGAEGRILTVGTSHEFLYORGSSYF 425
 Qy 422 SPALLYPMTVSNKATLHSPYTFNAFTRPGSIPQASARCPNSCVTVGYTDPYPLIFRYN 481
 Db 426 SPALLYPMTVSNKATLHSPYTFNAFTRPGSIPQASARCPNSCVTVGYTDPYPLIFRYN 485
 Qy 482 HTLRGVFGTMDSEQARLNPASAVFDSTSRIRTRVSSSTKAAYTTSTCFKVVTKNTKY 541
 Db 486 HTLRGVFGTMDSEQARLNPASAVFDSTSRIRTRVSSSTKAAYTTSTCFKVVTKNTKY 545
 Qy 542 CLSTIAEISNTLFGFERRIVPLVEILKNDGVREARSG 577
 Db 546 CLSTIAEISNTLFGFERRIVPLVEILKNDGVREARSG 581

RESULT 10

AAW10690
 ID AAW10690 standard; Protein; 581 AA.

AC AAW10690;
 XX
 DT 05-MAY-1997 (first entry)
 DT
 XX
 DE Newcastle disease virus haemagglutinin.
 DB
 XX Fowlpox virus; FPV; recombinant virus; vector; vaccine;
 KM immunisation; NDV; haemagglutinin; fusion protein; antigen;
 XX poultry.
 XX
 XX Newcastle disease virus.

PN MO640880-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 04-JUN-1996; 96MO-US11187.
 XX
 PR 07-JUN-1995; 95US-0484790.
 XX
 PA (SYTR) SYNTRIO CORP.
 XX
 PI Cochran MD, Junker DE, Singer PA;
 XX
 DR WPI; 1997-087060/08.
 XX
 DR N-PSDB; AAT48510.
 XX
 PT New recombinant fowlpox virus - contg. a foreign DNA sequence
 PT inserted into the fowlpox virus genome, used for the prodn. of
 PT vaccines.
 XX
 PS Disclosure; Page 107-108; 134pp; English.
 XX
 CC Newcastle disease virus (NDV) haemagglutinin (HN) (AAM10690) and
 CC fusion (F) protein (AAM10691) are expressed by novel recombinant
 CC fowlpox virus (FPV). The genes (see also AAT48510) for HN and F can
 CC be inserted into homology vector 443-88.8 (see also AAT48511) at the
 CC unique SfiI site, yielding homology vector 502-26.22 (see also
 CC AAT48502-05), which can be used to insert the NDV HN and F genes
 CC into fowlpox virus. The recombinant virus is used to deliver the
 CC vaccine antigens to poultry.
 XX
 SQ Sequence 581 AA;
 XX
 Query Match 97.2%; Score 2915; DB 18; Length 581;
 Best Local Similarity 96.9%; Pred. No. 7e-275;
 Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 XX
 QY 2 DRAVSQVLENDEREAKNTWRLIFRIALLTVTLATSVASLVSMGASTPSDLVGIP 61
 DB 6 DRAVSQVLENDEREAKNTWRLIFRIALLTVTLATSVASLVSMGASTPSDLVGIP 65
 XX
 QY 62 RISRAEKTITSAAGSNODVVDRIYQVLAESPLALNTETTMNATISLSTQINGAANS 121
 DB 66 RISRAEKTITSLGNSODVVDRIYQVLAESPLALNTETTMNATISLSTQINGAANS 125
 XX
 QY 122 GWGAPIHDPDFIGIGKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRIPEFDM 181
 DB 126 GWGAPIHDPDFIGIGKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRIPEFDM 185
 XX
 QY 182 ATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLISLDDTONRKS CSVS 241
 DB 186 ATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLISLDDTONRKS CSVS 245
 XX
 QY 242 ATPGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFGDWVANYPG 301
 DB 246 ATPGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFGDWVANYPG 305
 XX
 QY 302 VGGSSFLIDGVWFVSGIKPNPSDVTVOEGKYIYKRYNDTCPEDDYQIRMAKSSYKP 361
 DB 306 VGGSSFLIDSRWFVSGIKPNPSDVTVOEGKYIYKRYNDTCPEDDYQIRMAKSSYKP 365
 XX
 QY 362 GRFGKRIIOQAALISIKVTSIGEDPVLTPPNTVTLGAEGRIITVTSHFVLORGSSYF 421
 DB 366 GRFGKRIIOQAALISIKVTSIGEDPVLTPPNTVTLGAEGRIITVTSHFVLORGSSYF 425
 XX
 QY 422 SPALLYMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVYDPPYPLIFRYN 481
 DB 426 SPALLYMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVYDPPYPLIFRYN 485
 XX
 QY 482 HTLRGVGTMLDSDQALNPASAFDSTSRIRIVSSSSSTKAAVYTSSTCFKVKTKNTKY 541
 DB 486 HTLRGVGTMLDSDQALNPASAFDSTSRIRIVSSSSSTKAAVYTSSTCFKVKTKNTKY 545
 XX
 QY 542 CLSIAEISNTLFGFBRIVPLLVLEILKNDGVREARSG 577

DB 546 CLSIAEISNTLFGFBRIVPLLVLEILKNDGVREARSG 581
 RESULT 11
 AAY21982
 ID AAY21982 standard; Protein; 581 AA.
 XX
 AC AAY21982;
 XX
 DT 07-SEP-1999 (first entry)
 XX
 DE Seq ID No: 13 of US925358.
 XX
 KM Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;
 KM Newcastle disease virus; NDV; Fowlpox; Infectious Laryngotracheitis.
 XX
 OS Fowlpox virus.
 XX
 XX US925358-A.
 XX
 PD 20-JUL-1999.
 XX
 PF 07-JUN-1995; 95US-0484575.
 XX
 PR 07-JUN-1995; 95US-0484575.
 PR 26-FEB-1993; 93US-0024156.
 PR 28-FEB-1994; 94MO-US02252.
 XX
 PA (SYTR) SYNTRIO CORP.
 XX
 PI Cochran MD, Junker DE;
 XX
 DR WPI; 1999-418249/35.
 DR N-PSDB; AAX81147.
 XX
 PT Fowlpox viruses, useful as vaccines for immunization of
 PT chickens/turkeys against Fowlpox and Newcastle disease virus
 XX
 PS Disclosure; Column 61-70; 108pp; English.
 XX
 CC The invention relates to a recombinant fowlpox virus (FPV) comprising
 CC a foreign DNA inserted into a region of the fowlpox virus genome
 CC corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
 CC host cell. The virus is used as a vaccine for immunising chickens against
 CC Newcastle disease virus (NDV), Fowlpox, and Infectious Laryngotracheitis.
 XX
 SQ Sequence 581 AA;
 XX
 Query Match 97.2%; Score 2915; DB 20; Length 581;
 Best Local Similarity 96.9%; Pred. No. 7e-275;
 Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 XX
 QY 2 DRAVSQVLENDEREAKNTWRLIFRIALLTVTLATSVASLVSMGASTPSDLVGIP 61
 DB 6 DRAVSQVLENDEREAKNTWRLIFRIALLTVTLATSVASLVSMGASTPSDLVGIP 65
 XX
 QY 62 RISRAEKTITSAAGSNODVVDRIYQVLAESPLALNTETTMNATISLSTQINGAANS 121
 DB 66 RISRAEKTITSLGNSODVVDRIYQVLAESPLALNTETTMNATISLSTQINGAANS 125
 XX
 QY 122 GWGAPIHDPDFIGIGKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRIPEFDM 181
 DB 126 GWGAPIHDPDFIGIGKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRIPEFDM 185
 XX
 QY 182 ATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLISLDDTONRKS CSVS 241
 DB 186 ATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLISLDDTONRKS CSVS 245
 XX
 QY 242 ATPGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFGDWVANYPG 301
 DB 246 ATPGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFGDWVANYPG 305

QY 302 VGGSGFIDGRWFSYVGGGLKENSBDTVQEGKVIYKRYNDTCPEDDYQIRMAKSSYKP 361
DB 306 VGGGFFIDSRWFSYVGGGLKENTPBDTVQEGKVIYKRYNDTCPEDDYQIRMAKSSYKP 365
QY 362 GRFGGKRIQOAILSTIKYSTSLGEDPVLTPPNTVTLMAEGRIITVGTSHFLYORGSSYF 421
DB 366 GRFGGKRIQOAILSTIKYSTSLGEDPVLTPPNTVTLMAEGRIITVGTSHFLYORGSSYF 425
QY 422 SPALLPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFRYN 481
DB 426 SPALLPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFRYN 485
QY 482 HTLRGVEFTMLDSEQARLNPAASAVPDSRSRITRVSSSSSTKAAVYTSCTCKVVKTKNTY 541
DB 486 HTLRGVEFTMLDSEQARLNPAASAVPDSRSRITRVSSSSSTKAAVYTSCTCKVVKTKNTY 545
QY 542 CLSTIAEISNTLFGFRIYPLVLEILKNDGVREARSG 577
DB 546 CLSTIAEISNTLFGFRIYPLVLEILKNDGVREARSG 581

RESULT 12

AAB36038
ID AAB36038 standard; Protein; 581 AA.

AC AAB36038;
XX
DT 02-MAR-2001 (first entry)

DE Protein encoded by NDV Sfil fragment.

XX Fowlpox virus; FPV; antiviral; antibacterial; vaccine;
KW Newcastle's disease virus; NDV; Marek's disease;
XX infectious laryngotracheitis.

OS Newcastle's disease virus.

XX US6136318-A.

XX 24-OCT-2000.

XX 07-JUN-1995; 95US-0486414.

XX 26-FEB-1993; 93US-0024156.

XX 28-FEB-1994; 94WO-US02252.

PA (JUNK/) JUNKER D E.

PA (COCH/) COCHRAN M D.

PI Cochran MD, Junker DE;

XX MPI: 2000-686071/67.

XX N-PsDB; AAC67862.

XX New recombinant fowlpox virus useful as vaccines contains foreign DNA

XX inserted into specific non-essential region of the genome

XX Disclosure; Column 69-72; 56pp; English.

XX The present sequence is provided in a specification relating to a

XX recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted

XX within a 3.5 kb EcorI fragment of the FPV genomic DNA. The foreign DNA

XX can be expressed in host cells infected with FPV. The recombinant FPV

XX may be used in vaccines to protect animals (especially chickens) against

XX fowlpox and, depending on the source of the foreign DNA, other diseases,

XX particularly Newcastle's disease, Marek's disease or infectious

XX laryngotracheitis.

XX SQ Sequence 581 AA;

Query Match 97.2%; Score 2915; DB 21; Length 581;

Best Local Similarity 96.9%; Pred. No. 7e-275;

Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 DRAVSQVLENDEREAKNTWRLIFRIALLTVTLATSVASLYSMGASTPSDLVGIP 61
DB 6 DRAVSQVLENDEREAKNTWRLIFRIALLTVTLATSVASLYSMGASTPSDLVGIP 65
QY 62 RISRAEEKITSLAGSNQDVDRIRYQVALBESPLALNTETTITMAITSLSQINGAANS 121
DB 66 RISRAEEKITSLAGSNQDVDRIRYQVALBESPLALNTETTITMAITSLSQINGAANS 125
QY 122 GMGAPIHDPDIFIGIGELIYDNASDVTSPFSAFOEHLNFIPTGSGCTRIIPSPMS 181
DB 126 GMGAPIHDPDIFIGIGELIYDNASDVTSPFSAFOEHLNFIPTGSGCTRIIPSPMS 185
QY 182 ATHCYTHNVILSGCRDHSRSHQYALGVLTATGRIFFSTLRSISLDDTQNRKSCSVS 241
DB 186 ATHCYTHNVILSGCRDHSRSHQYALGVLTATGRIFFSTLRSISLDDTQNRKSCSVS 245
QY 242 ATPIGCDMLCSKATETEEDYNASVPTLMAHGRIGPDQYHEKLDVTTLFEDVANYPG 301
DB 246 ATPIGCDMLCSKATETEEDYNASVPTLMAHGRIGPDQYHEKLDVTTLFEDVANYPG 305
QY 302 VGGSGFIDGRWFSYVGGGLKENSBDTVQEGKVIYKRYNDTCPEDDYQIRMAKSSYKP 361
DB 306 VGGGFFIDSRWFSYVGGGLKENTPBDTVQEGKVIYKRYNDTCPEDDYQIRMAKSSYKP 365
QY 362 GRFGGKRIQOAILSTIKYSTSLGEDPVLTPPNTVTLMAEGRIITVGTSHFLYORGSSYF 421
DB 366 GRFGGKRIQOAILSTIKYSTSLGEDPVLTPPNTVTLMAEGRIITVGTSHFLYORGSSYF 425
QY 422 SPALLPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFRYN 481
DB 426 SPALLPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFRYN 485
QY 482 HTLRGVEFTMLDSEQARLNPAASAVPDSRSRITRVSSSSSTKAAVYTSCTCKVVKTKNTY 541
DB 486 HTLRGVEFTMLDSEQARLNPAASAVPDSRSRITRVSSSSSTKAAVYTSCTCKVVKTKNTY 545
QY 542 CLSTIAEISNTLFGFRIYPLVLEILKNDGVREARSG 577
DB 546 CLSTIAEISNTLFGFRIYPLVLEILKNDGVREARSG 581

RESULT 13

AAV58182
ID AAV58182 standard; Protein; 581 AA.

XX AAV58182;

DT 14-MAR-2000 (first entry)

DE NDV haemagglutinin-neuraminidase (HN).

XX Fowlpox virus; FPV; recombinant; antigenic protein; expression;

XX infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;

XX Marek's disease virus; cytokine; promoter; homologous recombination;

XX homology vector; multivalent; live vaccine; haemagglutinin;

XX neuraminidase.

XX Newcastle disease virus.

XX Key

XX Location/Qualifiers

XX Domain

XX US6001369-A.

XX 14-DEC-1999.

XX 07-JUN-1995; 95US-0477459.

XX 26-FEB-1993; 93US-0024156.

XX 28-FEB-1994; 94WO-US02252.

XX

PA (SYTR) SYNTRO CORP.
 XX
 PI Junker DE, Cochran MD;
 XX
 DR WPI, 2000-071638/06.
 DR N-PSDB; AA249295.
 XX
 PT Recombinant fowlpox virus useful as a vaccine for immunizing fowl
 PT against Marek's disease, Newcastle disease, infectious
 PT Laryngotracheitis virus and/or fowlpox
 XX
 PS Claim 5; Columns 69-72; 56pp; English.
 XX
 CC The invention relates to a recombinant fowlpox virus (FPV)
 CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment
 CC of the fowlpox virus genome. The foreign DNA is capable of being
 CC expressed in a host cell into which the fowlpox virus has been
 CC introduced and encodes an antigenic protein. The antigenic protein
 CC which may be expressed includes infectious laryngotracheitis virus
 CC (ILTIV) glycoprotein B (gB) or glycoprotein D (gD, AA58184), Newcastle
 CC disease virus (NDV) haemagglutinin (HN, AA58182) or fusion (F) protein
 CC (AA58183) and Marek's disease virus gB or gD. The foreign DNA may
 CC alternatively encode a cytokine such as chicken myelomonocytic growth
 CC factor (CMGF) or chicken interferon (cIFN). The foreign DNA in the
 CC recombinant FPV is under the control of one or more synthetic pox
 CC promoters, enabling control of strength and timing of heterologous
 CC gene expression. The synthetic pox virus promoters that may be used are
 CC based on promoters of the vaccinia virus and include early promoter 1
 CC (EP1), late promoter 1 (LP1), EP2 and LP2 (AA249291-249294,
 CC respectively). The recombinant FPV is generated via homologous
 CC recombination between FPV DNA and a homology vector containing the
 CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of
 CC the invention are used as multivalent live vaccines for immunising fowl
 CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The
 CC present sequence represents NDV haemagglutinin-neuraminidase (HN).
 XX
 SQ Sequence 581 AA;
 Query Match 97.2%; Score 2915; DB 21; Length 581;
 Best Local Similarity 96.9%; Pred. No. 7e-275; Indels 0; Gaps 0;
 Matches 558; Conservative 8; Mismatches 10;
 QY 2 DRAVSQVALENDEREAQNTWRLIFRIALLTVVTLATSVASLVSMGASTPSDLVGIP 61
 DB 6 DRAVSQVALENDEREAQNTWRLIFRIALLTVVTLATSVASLVSMGASTPSDLVGIP 65
 QY 62 RISRAEKITSAAGSNODVDRIRYQVALSPALNTETTINMAITSLSYQINGAANS 121
 DB 66 RISRAEKITSLTSGNODVDRIRYQVALSPALNTETTINMAITSLSYQINGAANS 125
 QY 122 GWAQPIHDPPIGIGIKELIVDNASDVTSFYPSPAFQEHNLPIPAPTTSGCCTRI 181
 DB 126 GWAQPIHDPPIGIGIKELIVDNASDVTSFYPSPAFQEHNLPIPAPTTSGCCTRI 185
 QY 182 ATHYCYTHNVILSGCRDSSHSHOYLALGVLTATGRIFFSTLRSISLDTQNRKSCSV 241
 DB 186 ATHYCYTHNVILSGCRDSSHSHOYLALGVLTATGRIFFSTLRSISLDTQNRKSCSV 245
 QY 242 ATPGCDMLCSKVTETEEDYNSAVPTLMAHGRIGPGQIHEKDLVTTLPEDVMANPG 301
 DB 246 ATPGCDMLCSKVTETEEDYNSAVPTLMAHGRIGPGQIHEKDLVTTLPEDVMANPG 305
 QY 302 VGGSSFLDGVWVPVVGGLKPNSPSDVORGKVIYRYVNDTCPEDEDYQIRMAKSSYK 361
 DB 306 VGGSSFLDGVWVPVVGGLKPNSPSDVORGKVIYRYVNDTCPEDEDYQIRMAKSSYK 365
 QY 362 GREGSKRIQQAISIKVSTLGEDEPVLTPPNTVTLMGAGRIILTVSTSHFLVORGSSYF 421
 DB 366 GREGSKRIQQAISIKVSTLGEDEPVLTPPNTVTLMGAGRIILTVSTSHFLVORGSSYF 425
 QY 422 SPALLVPMTVSNKTATLHSPYTNAFTPGSIPQASARCPNSCVTVGTYDPPYLFYRN 481
 DB 426 SPALLVPMTVSNKTATLHSPYTNAFTPGSIPQASARCPNSCVTVGTYDPPYLFYRN 485

QY 482 HTLRGVFGTMDSEQARLNPASAVFDPSTSRSRITRVSSSTKAAYTTSTCFKVKTKNTKY 541
 DB 486 HTLRGVFGTMDSEQARLNPASAVFDPSTSRSRITRVSSSTKAAYTTSTCFKVKTKNTKY 545
 QY 542 CLSIAEISNTLFGFEPRIVPLVLEILKNDGVREARSG 577
 DB 546 CLSIAEISNTLFGFEPRIVPLVLEILKNDGVREARSG 581
 RESULT 14
 ID AAP96147
 ID AAP96147 standard; protein; 616 AA.
 XX
 AC AAP96147;
 XX
 DT 25-MAR-2003 (updated)
 DT 21-JAN-1991 (first entry)
 XX
 DE Sequence of Newcastle disease virus (NDV) - derived haemagglutinin
 DE neuraminidase (HN).
 XX
 KM Fowlpox; vaccine.
 XX
 OS Newcastle disease virus.
 XX
 PN EP308220-A.
 XX
 PD 22-MAR-1989.
 XX
 PF 15-SEP-1988; 88EP-0308532.
 XX
 PR 16-SEP-1987; 87JP-0231653.
 PR 16-SEP-1988; 88JP-0231898.
 XX
 PA (JAPG) NIPPON ZEON KK.
 XX
 PI Yanagida N, Saeki S, Ogawa R, Kamogawa K, Hayashi Y, Sawaguchi K;
 XX
 DR WPI, 1989-087589/12.
 DR N-PSDB; AAN91000.
 XX
 PT Recombinant avipox virus used as vaccine for fowl -
 PT having inserted cDNA for Newcastle disease derived
 PT haemagglutinin neuraminidase
 XX
 PS Disclosure; Fig 4a-4e; 27pp; English.
 XX
 CC cDNA coding for NDV-derived HN prepared using D-26 strain includes two
 CC kinds, one of which is composed of 1746 bp from 112th to 1857th and
 CC another is composed of 1848 bp from 112th to 1959th.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 616 AA;
 Query Match 95.0%; Score 2847; DB 10; Length 616;
 Best Local Similarity 94.1%; Pred. No. 3.3e-268;
 Matches 543; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MDRAVSQVALENDEREAQNTWRLIFRIALLTVVTLATSVASLVSMGASTPSDLVGIP 60
 DB 1 MDRAVSQVALENDEREAQNTWRLIFRIALLTVVTLATSVASLVSMGASTPSDLVGIP 60
 QY 61 TRISRAEKITSAAGSNODVDRIRYQVALSPALNTETTINMAITSLSYQINGAANS 120
 DB 61 TRISRAEKITSAAGSNODVDRIRYQVALSPALNTETTINMAITSLSYQINGAANS 120
 QY 121 SCMGAPIHDPPIGIGIKELIVDNASDVTSFYPSPAFQEHNLPIPAPTTSGCCTRI 180
 DB 121 SCMGAPIHDPPIGIGIKELIVDNASDVTSFYPSPAFQEHNLPIPAPTTSGCCTRI 180
 QY 181 SATHYCYTHNVILSGCRDSSHSHOYLALGVLTATGRIFFSTLRSISLDTQNRKSCSV 240

Db 161 SATHCYTHNVLLSGCRDHS HQYLALGVLTATGRTAFSTLRSLINDDTQNRKSCSV 240
QY 241 SATPLGCDMLCSKYETEEDYNASAVPTLMAHGRGLGFDQYHEKDLDTYTLFEDWVANYP 300
Db 241 SATPLGCDMLCSKYETEEDYNASAIPTSMVHGRLGFDQYHEKDLDTYTLFEDWVANYP 300
QY 301 GVGGSFIDGRVWFVSYGGLKPNSSDPTVQEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360
Db 301 GVGGSFIDNRVWFVSYGGLKPNSSDPTAQEGKYVIYKRYNDTCDEDDYQIRMAKSSYK 360
QY 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPPNTVTLMAAGRGLITVGTSHFLYORGSSY 420
Db 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPPNTVTLMAAGRGLITVGTSHFLYORGSSY 420
QY 421 FSPALLYPMVTSNKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVTVYTDYPLFYR 480
Db 421 FSPALLYPMVTSNKTATLHSPYTFNAFTRPQSVPCQASARCPNSCVTVYTDYPLFYR 480
QY 481 NHTLRGVFTMLDSEQARLNPASAVFDSISRRTIRVSSSTKAAVTTSTCFKVKTKNT 540
Db 481 NHTLRGVFTMLDSEQARLNPASAVFDSISRRTIRVSSSTKAAVTTSTCFKVKTKNT 540
QY 541 YCLSTIAEISNTLFGFRIYVPLVLEILKDDGVREARSG 577
Db 541 YCLSTIAEISNTLFGFRIYVPLVLEILKDDGVREARSG 577

RESULT 15

AAR06329 standard; protein; 616 AA.

AAR06329;

18-DEC-1990 (first entry)

Newcastle disease virus haemagglutinin neuraminidase gene product.

Fowl pox virus; Newcastle disease antigen; vaccine;

haemagglutinin neuraminidase;

Newcastle disease virus.

W03007581-A.

12-JUL-1990.

28-DEC-1989; 89WO-J001330.

28-MAR-1989; 89JP-0076025.

29-DEC-1988; 88JP-0335605.

(JAFG) NIPPON ZEON KK.

Ogawa R, Yanagida N, Saeki S, Ohkawa S;

MPI, 1990-239051/31.

N-P8DB; AA005549.

Promoter DNA derived from avipox virus, and chimera gene - can be used to produce recombinant avipox virus for vaccine manufacture

Disclosure; Page ?; ?pp; Japanese.

Promoter fragment may be attached to a viral antigen, such as a Newcastle disease antigen eg Haemagglutinin neuraminidase. This may be expressed in a transformed host, to give a stabilised vaccine on a large scale.

See also AA005544-8.

Sequence 616 AA;

Query Match 94.7%; Score 2839; DB 11; Length 616;

Best Local Similarity 93.8%; Pred. No. 2e-267; Matches 541; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 1 MDRVSOVALNDRREANTRRLFRITALLTVVTLATSVASIVYSGASTPDIVGIP 60
Db 1 MDRVSOVALNDRREANTRRLFRITALLTVVTLATSVASIVYSGASTPDIVGIP 60
QY 61 TRISRAEKTISALGSNDVDRIYKOVALESPLALNTETITINMAISLSYQINGAANN 120
Db 61 TRISRAEKTISALGSNDVDRIYKOVALESPLALNTETITINMAISLSYQINGAANN 120
QY 121 SCGAPLHDPDFIGIGIKELIVDNASDVTSFYPAPFQEHNLFPAPTGGSCCTRIPSFDM 180
Db 121 SCGAPLHDPDFIGIGIKELIVDNASDVTSFYPAPFQEHNLFPAPTGGSCCTRIPSFDM 180
QY 181 SATHCYTHNVLLSGCRDHS HQYLALGVLTATGRTAFSTLRSLINDDTQNRKSCSV 240
Db 181 SATHCYTHNVLLSGCRDHS HQYLALGVLTATGRTAFSTLRSLINDDTQNRKSCSV 240
QY 241 SATPLGCDMLCSKYETEEDYNASAVPTLMAHGRGLGFDQYHEKDLDTYTLFEDWVANYP 300
Db 241 SATPLGCDMLCSKYETEEDYNASAIPTSMVHGRLGFDQYHEKDLDTYTLFEDWVANYP 300
QY 301 GVGGSFIDGRVWFVSYGGLKPNSSDPTVQEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360
Db 301 GVGGSFIDNRVWFVSYGGLKPNSSDPTAQEGKYVIYKRYNDTCDEDDYQIRMAKSSYK 360
QY 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPPNTVTLMAAGRGLITVGTSHFLYORGSSY 420
Db 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPPNTVTLMAAGRGLITVGTSHFLYORGSSY 420
QY 421 FSPALLYPMVTSNKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVTVYTDYPLFYR 480
Db 421 FSPALLYPMVTSNKTATLHSPYTFNAFTRPQSVPCQASARCPNSCVTVYTDYPLFYR 480
QY 481 NHTLRGVFTMLDSEQARLNPASAVFDSISRRTIRVSSSTKAAVTTSTCFKVKTKNT 540
Db 481 NHTLRGVFTMLDSEQARLNPASAVFDSISRRTIRVSSSTKAAVTTSTCFKVKTKNT 540
QY 541 YCLSTIAEISNTLFGFRIYVPLVLEILKDDGVREARSG 577
Db 541 YCLSTIAEISNTLFGFRIYVPLVLEILKDDGVREARSG 577

Search completed: January 2, 2004, 16:18:24
Job time : 59 secs

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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:52 ; Search time 28 Seconds

(without alignments)
1981.762 Million cell updates/sec

Title: US-09-915-515A-1

Perfect score: 2998
Sequence: 1 MDRVSGVALBNDREKNT.....IVPLVEILKNDGVEARSG 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2989	99.7	577	1 F46328	hemagglutinin-neur
2	2945	98.2	577	1 D46328	hemagglutinin-neur
3	2920	97.4	577	1 D46328	hemagglutinin-neur
4	2914	97.2	577	1 HNNZNC	hemagglutinin-neur
5	2913	97.2	577	1 E46328	hemagglutinin-neur
6	2871	95.8	616	1 E46328	hemagglutinin-neur
7	2862	95.5	616	1 HNNZU1	hemagglutinin-neur
8	2849	95.0	616	1 C46328	hemagglutinin-neur
9	2848	95.0	616	1 B46328	hemagglutinin-neur
10	2846	94.9	616	1 HNNZOD	hemagglutinin-neur
11	2763	92.2	571	1 A36829	hemagglutinin-neur
12	2759	92.0	571	1 I46328	hemagglutinin-neur
13	2758	92.0	571	1 B36829	hemagglutinin-neur
14	2751	91.8	571	1 H46328	hemagglutinin-neur
15	2746	91.6	571	2 S40164	hemagglutinin-neur
16	2738.5	91.3	570	1 HNNZAV	hemagglutinin-neur
17	2719.5	90.7	581	2 S45114	hemagglutinin-neur
18	2711	90.4	571	1 C36829	hemagglutinin-neur
19	2666	88.9	571	1 D36829	hemagglutinin-neur
20	842	28.1	576	2 B37483	HN protein - Muray
21	838	28.0	568	1 HNNZ41	hemagglutinin-neur
22	781	26.1	582	1 HNNZM4	hemagglutinin-neur
23	778	26.0	571	1 HNNZP2	hemagglutinin-neur
24	777	25.9	571	1 HNNZT2	hemagglutinin-neur
25	772	25.8	565	1 HNNZC3	hemagglutinin-neur
26	771	25.7	565	1 HNNZSV	hemagglutinin-neur
27	770	25.7	582	1 HNNZMP	hemagglutinin-neur
28	766	25.6	582	1 HNNZSB	hemagglutinin-neur
29	765	25.5	565	1 HNNZC1	hemagglutinin-neur

30	765	25.5	565	1 HNNZC2	hemagglutinin-neur
31	729	24.3	576	2 A45536	hemagglutinin-neur
32	689	23.0	573	1 HNNZ4A	hemagglutinin-neur
33	480	16.0	575	1 HNNZS2	hemagglutinin-neur
34	479	16.0	575	1 HNNZS8	hemagglutinin-neur
35	479	16.0	575	2 S14532	hemagglutinin-neur
36	467	15.6	575	2 S12335	hemagglutinin-neur
37	455.5	15.2	572	1 HNNZ73	hemagglutinin-neur
38	448.5	15.0	576	1 HNNZS5	hemagglutinin-neur
39	445.5	14.9	572	1 HNNZ82	hemagglutinin-neur
40	444.5	14.8	572	1 HNNZ80	hemagglutinin-neur
41	444	14.8	572	1 HNNZP3	hemagglutinin-neur
42	442.5	14.8	572	2 S37253	hemagglutinin-neur
43	441.5	14.7	572	1 HNNZB3	hemagglutinin-neur
44	441.5	14.7	572	1 HNNZ79	hemagglutinin-neur
45	441.5	14.7	575	2 A43487	hemagglutinin-neur

ALIGNMENTS

RESULT 1					
F46328 hemagglutinin-neuraminidase (EC 3.2.1.-) (version 1) - Newcastle disease virus					
C:Species: Newcastle disease virus					
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999					
C:Accession: F46328; A27005					
R:Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocentio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.					
Virology 169, 260-272, 1989					
A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari					
A:Reference number: A46328; MUID:89204897; PMID:2705297					
A:Accession: F46328					
A:Molecule type: mRNA					
A:Residues: 1-577 <SAK>					
A:Cross-References: GB:M24710, NID:g332339, PIDN:AAA46660.1, PID:g332340					
A:Experimental Source: strain BEA/45					
R:Miller, N.S.; Chamberg, P.; Emerson, P.T.					
J. Gen. Virol. 67, 1917-1927, 1986					
A:Title: Nucleotide sequence analysis of the hemagglutinin-neuraminidase gene of Newcast					
A:Reference number: A27005; MUID:8630666; PMID:3018130					
A:Accession: A27005					
A:Molecule type: mRNA					
A:Residues: 1-577 <ML>					
A:Cross-References: GB:X04355; GB:X03634; NID:g60935; PIDN:CAA27880.1; PID:g60936					
C:Genetics:					
A:Gene: HN					
C:Superfamily: Paramyxovirus hemagglutinin-neuraminidase					
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein					
F:2748/Domain: transmembrane #status predicted <TM>					
F:119,341,433,481,538/Binding site: carbohydrate (asn) (covalent) #status predicted					
Query Match					
Best Local Similarity 99.7%; Score 2989; DB 1; Length 577;					
Matches 575; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
Qy	1	MDRVSGVALBNDREKNTWRLIFRAILLTVLTATSVASIVYSGASTBSDLGIP	60		
Db	1	MDRVSGVALBNDREKNTWRLIFRAILLTVLTATSVASIVYSGASTBSDLGIP	60		
Qy	61	TRISRAEKITSAAGSNQDVDRIRYKQVLESPLALNTETTTMNAITSLSYOINGAAN	120		
Db	61	TRISRAEKITSAAGSNQDVDRIRYKQVLESPLALNTETTTMNAITSLSYOINGAAN	120		
Qy	121	SGWCAPIHDDPFGIGICEKELIVDNASVYTFYPSAFQEHNFIPAPTTGGCTRIPEFDM	180		
Db	121	SGWCAPIHDDPFGIGICEKELIVDNASVYTFYPSAFQEHNFIPAPTTGGCTRIPEFDM	180		
Qy	181	SATHYCYTHAVIISGCRDHSCHOYLALGVLRRTATGRIFPSTLRSTSLDTONRKSCSV	240		
Db	181	SATHYCYTHAVIISGCRDHSCHOYLALGVLRRTATGRIFPSTLRSTSLDTONRKSCSV	240		
Qy	241	SATPLGCDMLCSKYTEEBEDYNSAVFTLMAHRLGFGGYHEKDLVTTLFEDWVANYP	300		
Db	241	SATPLGCDMLCSKYTEEBEDYNSAVFTLMAHRLGFGGYHEKDLVTTLFEDWVANYP	300		

Db	241	SATLFGCDMLCSKXTEHEEDYNSAFTLMAHGLGDPGQYHEKDLDVTLTFEDWYANP	300
Qy	301	GVGGGSPFDGVMFVSVYCGLKPNSBDTVOEGKYVIYKRYNDTCPEDDYQIRMAKSSYK	360
Db	301	GVGGGSPFDGVMFVSVYCGLKPNSBDTVOEGKYVIYKRYNDTCPEDDYQIRMAKSSYK	360
Qy	361	PGREFGKKRIQOALISIKVSTSLGEDPVLVPEPNTVTLMGAGRLILTVGTSHFLLQRRSSY	420
Db	361	PGREFGKKRIQOALISIKVSTSLGEDPVLVPEPNTVTLMGAGRLILTVGTSHFLLQRRSSY	420
Qy	421	FSPALLYPMYISNKTATLHSPYTNAPFRPGSIPCOASARCPNSCVYTDYPIFYR	480
Db	421	FSPALLYPMYISNKTATLHSPYTNAPFRPGSIPCOASARCPNSCVYTDYPIFYR	480
Qy	481	NHTLRGVFGTILMDSEQARLNPASAVFDSTSRSRITRVSSTSKAAYTSTCFKVKVKNKT	540
Db	481	NHTLRGVFGTILMDSEQARLNPASAVFDSTSRSRITRVSSTSKAAYTSTCFKVKVKNKT	540
Qy	541	YCLSIATISNTLVFGSEFRIYVPLLVLEILKNDGYREARSG	577
Db	541	YCLSIATISNTLVFGSEFRIYVPLLVLEILKNDGYREARSG	577

RESULT 2

hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1996
C:Accession: G46328, A29201
R:Sasaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 260-272, 1989
A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence variation
A:Reference number: A46328, MUID:85204897, PMID:2705297
A:Accession: G46328
A:Molecule type: mRNA
A:Residues: 1-577 <SAB>
A:Cross-references: GB:M24711
A:Experimental source: strain TEX/48
R:Schäper, U.M.; Fuller, F.C.; Ward, M.D.W.; Mehrotra, Y.; Stone, H.O.; Stripp, B.R.; De
Virology 165, 291-295, 1988
A:Title: Nucleotide sequence of the envelope protein genes of a highly virulent, neurotropic
A:Reference number: A94379, MUID:88265873, PMID:3388773
A:Accession: A29201
A:Molecule type: tRNA
A:Residues: 1-577 <SCH>
A:Experimental source: strain Texas G.B.
C:Genetics:
A:Gene: HN
C:Superfamily: paramyxovirus hemagglutinin-neuraminidase
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydroxylase; transmembrane protein
/27-48/Domain: transmembrane #status predicted <TM>
/119,341,433,481,538/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 98.2%; Score 2945; DB 1; Length 577;

Best Local Similarity 98.1%; Pred. No. 1e-218;
Matches 566; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy	1	MDRAVSQYALNDEBEAKNTWRLIFRIALLTJVTLATSAVLVYSGASTPBDVIGIP	60
Qy	1	MDRAVSQYALNDEBEAKNTWRLIFRIALLTJVTLATSAVLVYSGASTPBDVIGIP	60
Db	1	MDRAVSQYALNDEBEAKNTWRLIFRIALLTJVTLATSAVLVYSGASTPBDVIGIP	60
Qy	61	TRISRAEKITSALGSNODVVDRIKYQVLESPLALNTETTIMAITSLSYQINGAANN	120
Db	61	TRISRAEKITSALGSNODVVDRIKYQVLESPLALNTETTIMAITSLSYQINGAANN	120
Qy	121	SGMGAPIHDPDPIGGIGKELIVDNASDVTSFYPSPAFOELNFIAPATTSGCTRI	180
Db	121	SGMGAPIHDPDPIGGIGKELIVDNASDVTSFYPSPAFOELNFIAPATTSGCTRI	180
Qy	121	SGMGAPIHDPDPIGGIGKELIVDNASDVTSFYPSPAFOELNFIAPATTSGCTRI	180
Db	121	SGMGAPIHDPDPIGGIGKELIVDNASDVTSFYPSPAFOELNFIAPATTSGCTRI	180
Qy	181	SATHCYTHANVILSGCRDHSHSYQYALGVLTATTATGRIFFSTLRISLDDTONRKSCSV	240
Db	181	SATHCYTHANVILSGCRDHSHSYQYALGVLTATTATGRIFFSTLRISLDDTONRKSCSV	240

QY	241	SATPILGCMLECKRMTETBEDYDINSAPVTLMAHRLGFDGQYHEKDLVTTLFEWVANYP	300
Db	241	SATPILGCMLECKRMTETBEDYDINSAPVTLMAHRLGFDGQYHEKDLVTTLFEWVANYP	300
QY	301	GVGGGSFLDGRVWFVSYYGLKPNSPEDTVQEGKVVYKRPNDICPEBODYQIRAKSSYK	360
Db	301	GVGGGSFLDGRVWFVSYYGLKPNSPEDTVQEGKVVYKRPNDICPEBODYQIRAKSSYK	360
QY	361	GRFGFGKTIQQAIIISIKVSTSLGDEPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY	420
Db	361	GRFGFGKTIQQAIIISIKVSTSLGDEPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY	420
QY	421	FSPALLYPMTVSNKTAATLHSPYTFNAFTRPGSIPQASARCPNCSVTVYTDPPYLFIYR	480
Db	421	FSPALLYPMTVSNKTAATLHSPYTFNAFTRPGSIPQASARCPNCSVTVYTDPPYLFIYR	480
QY	481	NHTLNGVFETMLDSEQARLNPAASAVFDSTSRKSIITRVSSSSTAAYTTSTCFKVVYKTKNT	540
Db	481	NHTLNGVFETMLDSEQARLNPAASAVFDSTSRKSIITRVSSSSTAAYTTSTCFKVVYKTKNT	540
QY	541	YCLSTAEISNTLFGERRIVPLVLEILKNDGVRARBG	577
Db	541	YCLSTAEISNTLFGERRIVPLVLEILKNDGVRARBG	577

RESULT 3

hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain BL/47)
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_Revision 31-Dec-1993 #text_change 15-Oct-1996
C:Accession: D46328
R:Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 260-272, 1989
A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence var
A:Reference number: A46328; NCID:89204897; PMID:2705257
A:Accession: D46328
A:Molecule type: mRNA
A:Residues: 1-577 <SA>
A:Cross-references: GB:M24708
C:GeneId:5
A:Gene: HN
C:Superfamily: paramyxovirus hemagglutinin-neuraminidase
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein
F:27-48/Domain: transmembrane #status predicted <TN>
F:119-341,433,481,538/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 97.4%; Score 2920; DB 1; Length 577;

Best Local Similarity 96.9%; Pred.No. 8,7e-21;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0.

QY	1	NRAVSQVLENDERAKKWTWRLIFRIATILLFVWTATVASIVYEMGASTPDLVIGP	60
Db	1	MDRAVSQVLENDERAKKWTWRLIFRIATILLFVWTATVASIVASLYEMGASTPDLVIGIP	60
QY	61	TRISRAEEKITSALGSDNODVDRIRYKQVAALESPLALINETTTINNAITSLSYQINGAANN	120
Db	61	TRISRAEEKITSSTLGSNDVVDRIYKQVAALESPLALINETTTINNAITSLSYQINGAANN	120
QY	121	SGMGAPIHHPDPLIGIGKELIYDNASDVTSFYPSAPOEHLNFIPIAPTGSCTRIIPSPDM	180
Db	121	SGMGAPIHHPDPIIGIGKELIYDNASDVTSFYPSAPOEHLNFIPIAPTGSCTRIIPSPDM	180
QY	181	SATHYCYTHNVILSGCRDHSHSQYIALGVLRITATGRIFFSTLRSISLDDTONRKSCSV	240
Db	181	SATHYCYTHNVILSGCRDHSHSQYIALGVLRISATGRVFFSTLRSINLDDTONRKSCSV	240
QY	241	SATPLGCDMLCSKRVETEEDNVNSAVPTLMAHRLGPDGOYHEKDVLVTTLFEEDVNAVYP	300
Db	241	SATPLGCDMLCSKARITEEDDINSAVPTRMVHRLGPDGOYHEKDVLVTTLFGDVMNAVYP	300
QY	301	GVGGGSFTIDGRWFSVYVGLKPNSPSDTVQEGKXVIYKRNVNDTCPDEODVQIRMAKSSYK	360
Db	301	GVGGGSFIDSRWFSVYVGLKPNTPSDTVQEGKXVIYKRNVNDTCPDEODVQIRMAKSSYK	360

```
OY 361 PGRFGKRIQOAILSIKVSISLGEDPVLTVPPNTVTLTGAGGRILTVGTSHFLYORGSSY 420
Db 361 PGRFGKRIQOAILSIKVSISLGEDPVLTVPPNTVTLTGAGGRILTVGTSHFLYORGSSY 420
OY 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
Db 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
OY 481 NHTLRGVFGTMDSEQARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKTKT 540
Db 481 NHTLRGVFGTMDSEQARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKTKT 540
OY 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577
```

RESULT 4

```
hemagglutinin-neuraminidase (EC 3.2.1.-) (version 2) - Newcastle disease virus
C/Species: Newcastle disease virus
C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
C/Accession: A26355
R/Jorgensen, E.D.; Collins, P.L.; Lomedico, P.T.
Virology 156, 12-24, 1987
A/Title: Cloning and nucleotide sequence of Newcastle disease virus hemagglutinin-neuram
A/Reference number: A26355; MUID:87122141; PMID:3027962
A/Accession: A26355
A/Molecule type: mRNA
A/Residues: 1-577 <JOK>
A/Cross-references: GB:M16573; NID:G332355; PID:AAA46668.1; PID:G332356
C/Genetics:
A/Gene: HN
C/Superfamily: paramyxovirus hemagglutinin-neuraminidase
C/Keywords: glycoprotein, glycosidase, hemagglutinin, hydrolase, transmembrane protein
F:27-50/Domain: transmembrane #status predicted <TM>
F:119,341,433,481,538/Binding site: carbohydrate (Asn) (covalent) #status predicted
```

Query Match 97.2%; Score 2914; DB 1; Length 577;

Best Local Similarity 96.7%; Pred. No. 2.5e-216; Matches 558; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

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OY 1 MDRASQVLENDREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPDLVIGIP 60
Db 1 MDRASQVLENDREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPDLVIGIP 60
OY 61 TRISRAEKTISALGSNODVVDRIYKOVALESPALLNTETTINMAITSLSYQINGAANN 120
Db 61 TRISRAEKTISALGSNODVVDRIYKOVALESPALLNTETTINMAITSLSYQINGAANN 120
OY 121 SGWAPLHDPDPIGIGIKELIVDASDVTSFYPSAFQEHNLFIAPPTGSGCTRIPSFDM 180
Db 121 SGWAPLHDPDPIGIGIKELIVDASDVTSFYPSAFQEHNLFIAPPTGSGCTRIPSFDM 180
OY 181 SATHYCYTHNVILSGCRDHSYQYLAGVLRRTATGRIFPSTLRSISLDTQNRKSCSV 240
Db 181 SATHYCYTHNVILSGCRDHSYQYLAGVLRRTATGRIFPSTLRSISLDTQNRKSCSV 240
OY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGLGPDQYHEKLDVTTLFEEDVANYP 300
Db 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGLGPDQYHEKLDVTTLFEEDVANYP 300
OY 301 GVGGSFIDGKRVMSVYVGLKPNPSPTVOEGKVIYKRYNDTPEDDQYQIRAKSSYK 360
Db 301 GVGGSFIDGKRVMSVYVGLKPNPSPTVOEGKVIYKRYNDTPEDDQYQIRAKSSYK 360
OY 361 PGRFGKRIQOAILSIKVSISLGEDPVLTVPPNTVTLTGAGGRILTVGTSHFLYORGSSY 420
Db 361 PGRFGKRIQOAILSIKVSISLGEDPVLTVPPNTVTLTGAGGRILTVGTSHFLYORGSSY 420
OY 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
Db 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
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Db 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
OY 481 NHTLRGVFGTMDSEQARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKTKT 540
Db 481 NHTLRGVFGTMDSEQARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKTKT 540
OY 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577
```

RESULT 5

```
hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain IAS/46)
C/Species: Newcastle disease virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1996
C/Accession: E46328
R/Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 260-272, 1989
A/Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari
A/Reference number: E46328; MUID:89204897; PMID:2705297
A/Accession: E46328
A/Molecule type: mRNA
A/Residues: 1-577 <SAK>
A/Cross-references: GB:M24709
C/Genetics:
A/Gene: HN
C/Superfamily: paramyxovirus hemagglutinin-neuraminidase
C/Keywords: glycoprotein, glycosidase, hemagglutinin, hydrolase, transmembrane protein
F:27-48/Domain: transmembrane #status predicted <TM>
F:119,341,433,481,538/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Query Match 97.2%; Score 2913; DB 1; Length 577;

Best Local Similarity 96.9%; Pred. No. 3e-216; Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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OY 1 MDRASQVLENDREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPDLVIGIP 60
Db 1 MDRASQVLENDREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPDLVIGIP 60
OY 61 TRISRAEKTISALGSNODVVDRIYKOVALESPALLNTETTINMAITSLSYQINGAANN 120
Db 61 TRISRAEKTISALGSNODVVDRIYKOVALESPALLNTETTINMAITSLSYQINGAANN 120
OY 121 SGWAPLHDPDPIGIGIKELIVDASDVTSFYPSAFQEHNLFIAPPTGSGCTRIPSFDM 180
Db 121 SGWAPLHDPDPIGIGIKELIVDASDVTSFYPSAFQEHNLFIAPPTGSGCTRIPSFDM 180
OY 181 SATHYCYTHNVILSGCRDHSYQYLAGVLRRTATGRIFPSTLRSISLDTQNRKSCSV 240
Db 181 SATHYCYTHNVILSGCRDHSYQYLAGVLRRTATGRIFPSTLRSISLDTQNRKSCSV 240
OY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGLGPDQYHEKLDVTTLFEEDVANYP 300
Db 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGLGPDQYHEKLDVTTLFEEDVANYP 300
OY 301 GVGGSFIDGKRVMSVYVGLKPNPSPTVOEGKVIYKRYNDTPEDDQYQIRAKSSYK 360
Db 301 GVGGSFIDGKRVMSVYVGLKPNPSPTVOEGKVIYKRYNDTPEDDQYQIRAKSSYK 360
OY 361 PGRFGKRIQOAILSIKVSISLGEDPVLTVPPNTVTLTGAGGRILTVGTSHFLYORGSSY 420
Db 361 PGRFGKRIQOAILSIKVSISLGEDPVLTVPPNTVTLTGAGGRILTVGTSHFLYORGSSY 420
OY 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
Db 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
OY 481 NHTLRGVFGTMDSEQARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKTKT 540
Db 481 NHTLRGVFGTMDSEQARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKTKT 540
OY 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577
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|||||
Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

RESULT 6

A46328 hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain D26/76)

C/Species: Newcastle disease virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999

C/Accession: A46328

R/Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.

Virol. 169, 260-272, 1989

A/Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari

A/Reference number: A46328; MUID:89204897; PMID:2705297

A/Accession: A46328

A/Molecule type: mRNA

A/Residues: 1-616 <S&K>

A/Cross-references: GB:M24705; NID:g332329; PIDN:AAA46655.1; PID:g332330

C/Genetics:

A/Gene: HN

C/Superfamily: paramyxovirus hemagglutinin-neuraminidase

C/Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein

P:27-48/Domain: transmembrane #status predicted <TM>

P:119,341,433,481,538,600/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.8%; Score 2871; DB 1; Length 616;

Best Local Similarity 94.6%; Pred. No. 5,76-213;

Matches 546; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60
1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

61 TRISRAEEKITSLGSDVNDVRIYKQVALESPALINTEITMNTSLSYQINGAAN 120

61 TRISRAEEKITSLGSDVNDVRIYKQVALESPALINTEITMNTSLSYQINGAAN 120

121 SGWGAPIHDPDITGIGKELIVNADSDVTSFYPSAFQEHINFTIPATTSGGCTRIIPSPDM 180

121 SGWGAPIHDPDITGIGKELIVNADSDVTSFYPSAFQEHINFTIPATTSGGCTRIIPSPDM 180

181 SATHYCYTHNVILSGCRDHS HQYLALGVLTATGRVFFSTLRSINLDDTONRKSCSV 240

181 SATHYCYTHNVILSGCRDHS HQYLALGVLTATGRVFFSTLRSINLDDTONRKSCSV 240

241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGRIGFDQYHEKLDVTTLPEDWVANYP 300

241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGRIGFDQYHEKLDVTTLPEDWVANYP 300

301 GVGGSFIDGRWVFSYVGGKLPNSPDTVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360

301 GVGGSFIDGRWVFSYVGGKLPNSPDTVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360

361 PGRFGGRVQQAIIISIKVSTSLGSDPVLTPPNTVTLMGAEGRVLTGTSHPFYQSGSSY 420

361 PGRFGGRVQQAIIISIKVSTSLGSDPVLTPPNTVTLMGAEGRVLTGTSHPFYQSGSSY 420

421 FSPALLYPMVNSKNTATLHSPYTFNAFTRPGSVPCQASARCNSCVTGVTDPYPLVFR 480

421 FSPALLYPMVNSKNTATLHSPYTFNAFTRPGSVPCQASARCNSCVTGVTDPYPLVFR 480

481 NHTLRGVFGTMDSEQARLNPAVAFPDSTRSRITRVSSSTKAAYTSTCFKVVTKNTK 540

481 NHTLRGVFGTMDSEQARLNPAVAFPDSTRSRITRVSSSTKAAYTSTCFKVVTKNTK 540

541 YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

541 YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

C/Species: Newcastle disease virus
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C/Accession: B23823
R/Millar, N.S.; Chambers, P.; Emerson, P.T.
J. Gen. Virol. 69, 613-620, 1988
A/Title: Nucleotide sequence of the fusion and hemagglutinin-neuraminidase glycoprotein
ns.
A/Reference number: A92799; MUID:88171450; PMID:3351479

A/Accession: B23823

A/Molecule type: mRNA

A/Residues: 1-616 <ML>

A/Cross-references: GB:D00243; NID:g222174; PIDN:BA00174.1; PID:g222176

C/Genetics:

A/Gene: HN

C/Superfamily: paramyxovirus hemagglutinin-neuraminidase

C/Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein

P:27-54/Domain: transmembrane #status predicted <TM>

P:119,341,433,481,538,600/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.5%; Score 2862; DB 1; Length 616;
Best Local Similarity 94.3%; Pred. No. 2,86-212;
Matches 544; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60
1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

61 TRISRAEEKITSLGSDVNDVRIYKQVALESPALINTEITMNTSLSYQINGAAN 120

61 TRISRAEEKITSLGSDVNDVRIYKQVALESPALINTEITMNTSLSYQINGAAN 120

121 SGWGAPIHDPDITGIGKELIVNADSDVTSFYPSAFQEHINFTIPATTSGGCTRIIPSPDM 180

121 SGWGAPIHDPDITGIGKELIVNADSDVTSFYPSAFQEHINFTIPATTSGGCTRIIPSPDM 180

181 SATHYCYTHNVILSGCRDHS HQYLALGVLTATGRVFFSTLRSINLDDTONRKSCSV 240

181 SATHYCYTHNVILSGCRDHS HQYLALGVLTATGRVFFSTLRSINLDDTONRKSCSV 240

241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGRIGFDQYHEKLDVTTLPEDWVANYP 300

241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGRIGFDQYHEKLDVTTLPEDWVANYP 300

301 GVGGSFIDGRWVFSYVGGKLPNSPDTVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360

301 GVGGSFIDGRWVFSYVGGKLPNSPDTVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360

361 PGRFGGRVQQAIIISIKVSTSLGSDPVLTPPNTVTLMGAEGRVLTGTSHPFYQSGSSY 420

361 PGRFGGRVQQAIIISIKVSTSLGSDPVLTPPNTVTLMGAEGRVLTGTSHPFYQSGSSY 420

421 FSPALLYPMVNSKNTATLHSPYTFNAFTRPGSVPCQASARCNSCVTGVTDPYPLVFR 480

421 FSPALLYPMVNSKNTATLHSPYTFNAFTRPGSVPCQASARCNSCVTGVTDPYPLVFR 480

481 NHTLRGVFGTMDSEQARLNPAVAFPDSTRSRITRVSSSTKAAYTSTCFKVVTKNTK 540

481 NHTLRGVFGTMDSEQARLNPAVAFPDSTRSRITRVSSSTKAAYTSTCFKVVTKNTK 540

541 YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

541 YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

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Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

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Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

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Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

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Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

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Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

Db YCISIAEISNTLFGFRIPLVLEILKDDGVREARSG 577

A:Reference number: A46328; MUID:89204897; PMID:2705297
A:Accession: C46328
A:Molecule type: mRNA
A:Residues: 1-616 <SAK>
A:Cross-references: GB:M24707
C:Genetics:
A:Gene: HN
C:Superfamily: paramyxovirus hemagglutinin-neuraminidase
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein
F:27-48/Domain: transmembrane #status predicted <TM>
F:119,341,433,481,538,600/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 95.0%; Score 2849; DB 1; Length 616;
Best Local Similarity 93.9%; Pred. No. 2.8e-211;
Matches 542; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDRASQVLENDREAKNTWRLFRIALLLTVTLATSVASLYVSGASTPSDLVIGP 60
DB 1 MDRASQVLENDREAKNTWRLFRIALLLTVTLATSVASLYVSGASTPSDLVIGP 60
QY 61 TRISRAEEKITSALGSNDVDRIYKQVLESPLALNTETTIMAITSLSYQINGANN 120
DB 61 TRISRAEEKITSALGSNDVDRIYKQVLESPLALNTETTIMAITSLSYQINGANN 120
QY 121 SGWGAPIHDPDPIGGIGKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
DB 121 SGWGAPIHDPDPIGGIGKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
QY 121 SGCGAPIHDPDPIGGIGKELIVDASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
DB 121 SGCGAPIHDPDPIGGIGKELIVDASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
QY 181 SATHYCTHNVILSGCRDHS HQYLAAGVLTATGRIFPSTLRSLDTONRKS CV 240
DB 181 SATHYCTHNVILSGCRDHS HQYLAAGVLTATGRIFPSTLRSLDTONRKS CV 240
QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFPGQVHEKDLDTTLFEDWVANYP 300
DB 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFPGQVHEKDLDTTLFEDWVANYP 300
QY 301 GVGGSFIDRGVWFSVYGGILKPNSPSDTVQEGKYVIYKRYNDTCPEBDYQIRMAKSSYK 360
DB 301 GVGGSFIDRGVWFSVYGGILKPNSPSDTVQEGKYVIYKRYNDTCPEBDYQIRMAKSSYK 360
QY 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPNTVTLMGAGRIITVGTSHFLYORGSSY 420
DB 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPNTVTLMGAGRIITVGTSHFLYORGSSY 420
QY 421 FSPALLYPMVTYSNKTAATLHSPYFNAPTRPGSIPCOASARCPNSCVTVYDPPPLVYR 480
DB 421 FSPALLYPMVTYSNKTAATLHSPYFNAPTRPGSIPCOASARCPNSCVTVYDPPPLVYR 480
QY 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRSTRIRVSSSTKAAVTTSTCFKVKTKNT 540
DB 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRSTRIRVSSSTKAAVTTSTCFKVKTKNT 540
QY 541 YCLSLAIISNTLFGFRIIVPLVLEILKNDGVREARS 577
DB 541 YCLSLAIISNTLFGFRIIVPLVLEILKNDGVREARS 577

RESULT 9
B46328 hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain QNE/66)
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
R:Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 260-272, 1989
A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence var
A:Reference number: A46328; MUID:89204897; PMID:2705297
A:Accession: B46328
A:Molecule type: mRNA
A:Residues: 1-616 <SAK>
A:Cross-references: GB:M24706; NID:9332331; PID:AAAA46654.1; PID:9332332
C:Genetics:
A:Gene: HN

C:Superfamily: paramyxovirus hemagglutinin-neuraminidase
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein
F:27-48/Domain: transmembrane #status predicted <TM>
F:119,341,433,481,538,600/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 95.0%; Score 2848; DB 1; Length 616;
Best Local Similarity 94.1%; Pred. No. 3.3e-211;
Matches 542; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 1 MDRASQVLENDREAKNTWRLFRIALLLTVTLATSVASLYVSGASTPSDLVIGP 60
DB 1 MDRASQVLENDREAKNTWRLFRIALLLTVTLATSVASLYVSGASTPSDLVIGP 60
QY 61 TRISRAEEKITSALGSNDVDRIYKQVLESPLALNTETTIMAITSLSYQINGANN 120
DB 61 TRISRAEEKITSALGSNDVDRIYKQVLESPLALNTETTIMAITSLSYQINGANN 120
QY 121 SGWGAPIHDPDPIGGIGKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
DB 121 SGWGAPIHDPDPIGGIGKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
QY 121 SGCGAPIHDPDPIGGIGKELIVDASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
DB 121 SGCGAPIHDPDPIGGIGKELIVDASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
QY 181 SATHYCTHNVILSGCRDHS HQYLAAGVLTATGRIFPSTLRSLDTONRKS CV 240
DB 181 SATHYCTHNVILSGCRDHS HQYLAAGVLTATGRIFPSTLRSLDTONRKS CV 240
QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFPGQVHEKDLDTTLFEDWVANYP 300
DB 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFPGQVHEKDLDTTLFEDWVANYP 300
QY 301 GVGGSFIDRGVWFSVYGGILKPNSPSDTVQEGKYVIYKRYNDTCPEBDYQIRMAKSSYK 360
DB 301 GVGGSFIDRGVWFSVYGGILKPNSPSDTVQEGKYVIYKRYNDTCPEBDYQIRMAKSSYK 360
QY 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPNTVTLMGAGRIITVGTSHFLYORGSSY 420
DB 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPNTVTLMGAGRIITVGTSHFLYORGSSY 420
QY 421 FSPALLYPMVTYSNKTAATLHSPYFNAPTRPGSIPCOASARCPNSCVTVYDPPPLVYR 480
DB 421 FSPALLYPMVTYSNKTAATLHSPYFNAPTRPGSIPCOASARCPNSCVTVYDPPPLVYR 480
QY 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRSTRIRVSSSTKAAVTTSTCFKVKTKNT 540
DB 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRSTRIRVSSSTKAAVTTSTCFKVKTKNT 540
QY 541 YCLSLAIISNTLFGFRIIVPLVLEILKNDGVREARS 576
DB 541 YCLSLAIISNTLFGFRIIVPLVLEILKNDGVREARS 576

RESULT 10
HNNZOD hemagglutinin-neuraminidase (EC 3.2.1.-) precursor - Newcastle disease virus (strain Quee
C:Species: Newcastle disease virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
R:Gorman, V.J.; Nestorowicz, A.; Mitchell, S.J.; Corino, G.L.; Sellack, P.W.
J. Biol. Chem. 263, 12522-12531, 1988
A:Title: Characterization of the sites of proteolytic activation of Newcastle disease vi
A:Reference number: A92665; MUID:88315049; PMID:3045120
A:Accession: A31110
A:Molecule type: genomic RNA
A:Residues: 1-616 <GOK>
A:Cross-references: GB:U03911; NID:9332327; PID:AAAA46654.1; PID:9332328
C:Genetics:
A:Gene: HN
C:Superfamily: paramyxovirus hemagglutinin-neuraminidase
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein
F:11-574/Product: hemagglutinin-neuraminidase #status predicted <HNS>
F:27-54/Domain: transmembrane #status predicted <TM>
F:119,341,433,481,538,600/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 94.9%; Score 2846; DB 1; Length 616;

[illegible][illegible]

QY 181 SATHYCYTHANVILSGCRDHSYQYALGVLRRTATGRIFFSTLRSLDTONRKS CV 240
 DB 181 SATHYCYTHANVILSGCRDHSYQYALGVLRRTATGRIFFSTLRSLDTONRKS CV 240
 QY 241 SATPLGCMCCKSKYTEREEDYNSAVPTLMAGLGFQYHEKDLYTLFEDVANYP 300
 DB 241 SATPLGCMCCKSKYTEREEDYNSAVPTLMAGLGFQYHEKDLYTLFEDVANYP 300
 QY 301 GVGGGSLFDGRWPSVYGLKPNPSDPTVQEGKVIYKRYNDTCPEDDOYIRMAKSSYK 360
 DB 301 GVGGGSLFDGRWPSVYGLKPNPSDPTVQEGKVIYKRYNDTCPEDDOYIRMAKSSYK 360
 QY 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPPNTVTLMAGRGLTVGTSHEFLYORGSSY 420
 DB 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPPNTVTLMAGRGLTVGTSHEFLYORGSSY 420
 QY 421 FSPALLPMTVNSKNTATLHSPYTFNAFTPFGSIPCOASARCPNCSVTGVYDPPVLFYR 480
 DB 421 FSPALLPMTVNSKNTATLHSPYTFNAFTPFGSIPCOASARCPNCSVTGVYDPPVLFYR 480
 QY 481 NHTLRGVFGTMDSEQARLNPAFAFDSTSRRTIRVSSSTKAAVTTSTCFKVKTKNT 540
 DB 481 NHTLRGVFGTMDSEQARLNPAFAFDSTSRRTIRVSSSTKAAVTTSTCFKVKTKNT 540
 QY 541 YCLSIABISNTLFGFEPRIVPLVLEILKNDGV 571
 DB 541 YCLSIABISNTLFGFEPRIVPLVLEILKNDGV 571

RESULT 13

hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus

C:Species: Newcastle disease virus
 C:Date: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
 C:Accession: S07126; B36829
 R:Womers, C.D.; de Henau, S.; Neyt, C.; Ebpion, D.; Letellier, C.; Meulemans, G.; Burny, Arch. Virol. 97, 101-113, 1987
 A:Title: The hemagglutinin-neuraminidase (HN) gene of Newcastle disease virus strain Ita
 A:Reference number: S07126; MUID:88076411; PMID:3318761
 A:Accession: S07126
 A:Molecule type: mRNA
 A:Residues: 1-571 <MEM>
 A:Cross-references: EMBL:M16640; NID:G332361; PIDN:AAA46671.1; PID:G332362
 R:Experimental source: strain Italien
 R:Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Negai, Y. Virology 169, 260-272, 1989
 A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence var
 A:Reference number: A46328; MUID:89204897; PMID:2705297
 A:Accession: B36829
 A:Molecule type: mRNA
 A:Residues: 1-2, 'LP', 5-52, 'S', 54-215, 'A', 217-399, 'AD', 402-571 <SAK>
 A:Cross-references: GB:M24715
 A:Experimental source: strain ITA/45
 C:Genetics: HN
 C:Superfamily: paramyxovirus hemagglutinin-neuraminidase
 C:Keywords: glycoprotein, glycosidase, hemagglutinin, hydrolase, transmembrane protein
 F:27-48/Domain: transmembrane #status predicted <TM>
 F:119,341,433,481,508,538/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.0%; Score 2758; DB 1; Length 571;

Best Local Similarity 91.1%; Pred. No. 2.6e-204; Indels 0; Gaps 0;

Matches 520; Conservative 25; Mismatches 26; Indels 0; Gaps 0;
 QY 1 MDRASQVAVLENDEREAKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPSDLVGP 60
 DB 1 MDRASQVAVLENDEREAKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPSDLVGP 60
 QY 61 TRIRAEKITSALGSNDVVDRIYKQVAVLESPALANTETTINMATISLSYQINGANN 120
 DB 61 TRIRAEKITSALGSNDVVDRIYKQVAVLESPALANTETTINMATISLSYQINGANN 120
 QY 181 SATHYCYTHANVILSGCRDHSYQYALGVLRRTATGRIFFSTLRSLDTONRKS CV 240
 DB 181 SATHYCYTHANVILSGCRDHSYQYALGVLRRTATGRIFFSTLRSLDTONRKS CV 240

QY 121 SGWAPLHDPDFIGGIGKEILVDNASDVTSFYPASFOEHLNFIAPPTGSGCTRI PFEDM 180
 DB 121 SGWAPLHDPDFIGGIGKEILVDNASDVTSFYPASFOEHLNFIAPPTGSGCTRI PFEDM 180
 QY 181 SATHYCYTHANVILSGCRDHSYQYALGVLRRTATGRIFFSTLRSLDTONRKS CV 240
 DB 181 SATHYCYTHANVILSGCRDHSYQYALGVLRRTATGRIFFSTLRSLDTONRKS CV 240
 QY 241 SATPLGCMCCKSKYTEREEDYNSAVPTLMAGLGFQYHEKDLYTLFEDVANYP 300
 DB 241 SATPLGCMCCKSKYTEREEDYNSAVPTLMAGLGFQYHEKDLYTLFEDVANYP 300
 QY 301 GVGGGSLFDGRWPSVYGLKPNPSDPTVQEGKVIYKRYNDTCPEDDOYIRMAKSSYK 360
 DB 301 GVGGGSLFDGRWPSVYGLKPNPSDPTVQEGKVIYKRYNDTCPEDDOYIRMAKSSYK 360
 QY 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPPNTVTLMAGRGLTVGTSHEFLYORGSSY 420
 DB 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPPNTVTLMAGRGLTVGTSHEFLYORGSSY 420
 QY 421 FSPALLPMTVNSKNTATLHSPYTFNAFTPFGSIPCOASARCPNCSVTGVYDPPVLFYR 480
 DB 421 FSPALLPMTVNSKNTATLHSPYTFNAFTPFGSIPCOASARCPNCSVTGVYDPPVLFYR 480
 QY 481 NHTLRGVFGTMDSEQARLNPAFAFDSTSRRTIRVSSSTKAAVTTSTCFKVKTKNT 540
 DB 481 NHTLRGVFGTMDSEQARLNPAFAFDSTSRRTIRVSSSTKAAVTTSTCFKVKTKNT 540
 QY 541 YCLSIABISNTLFGFEPRIVPLVLEILKNDGV 571
 DB 541 YCLSIABISNTLFGFEPRIVPLVLEILKNDGV 571

RESULT 14

hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain AUS/32)

C:Species: Newcastle disease virus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1996
 C:Accession: H46328
 R:Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Negai, Y. Virology 169, 260-272, 1989
 A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence var
 A:Reference number: A46328; MUID:89204897; PMID:2705297
 A:Accession: H46328
 A:Molecule type: mRNA
 A:Residues: 1-571 <SAK>
 A:Cross-references: GB:M24712
 C:Genetics: HN
 C:Superfamily: paramyxovirus hemagglutinin-neuraminidase
 C:Keywords: glycoprotein, glycosidase, hemagglutinin, hydrolase, transmembrane protein
 F:27-48/Domain: transmembrane #status predicted <TM>
 F:119,341,433,481,508,538/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.8%; Score 2751; DB 1; Length 571;

Best Local Similarity 91.4%; Pred. No. 8.8e-204; Indels 0; Gaps 0;

Matches 522; Conservative 23; Mismatches 26; Indels 0; Gaps 0;
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 DB 1 MDRASQVAVLENDEREAKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPSDLVGP 60
 QY 61 TRIRAEKITSALGSNDVVDRIYKQVAVLESPALANTETTINMATISLSYQINGANN 120
 DB 61 TRIRAEKITSALGSNDVVDRIYKQVAVLESPALANTETTINMATISLSYQINGANN 120
 QY 121 SGWAPLHDPDFIGGIGKEILVDNASDVTSFYPASFOEHLNFIAPPTGSGCTRI PFEDM 180
 DB 121 SGWAPLHDPDFIGGIGKEILVDNASDVTSFYPASFOEHLNFIAPPTGSGCTRI PFEDM 180
 QY 181 SATHYCYTHANVILSGCRDHSYQYALGVLRRTATGRIFFSTLRSLDTONRKS CV 240
 DB 181 SATHYCYTHANVILSGCRDHSYQYALGVLRRTATGRIFFSTLRSLDTONRKS CV 240

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QY 241 SATPLGCDMLCSKYTEETEEDYNASAVPTLMAHGRIGFQYHEKDLVTTLFEDWVANYP 300
DB 241 SATPLGCDMLCSKYTEETEEDYNASAVPTLMAHGRIGFQYHEKDLVTTLFEDWVANYP 300
QY 301 GVGGSFIDRWFVSYGGLKPNSPSDTVOEGKVYIKRYNDTCPPBODYQIIMAKSSYK 360
DB 301 GVGGSFIDRWFVSYGGLKPNSPSDTVOEGKVYIKRYNDTCPPBODYQIIMAKSSYK 360
QY 361 PGRFGKRVQOAILSIKVSFSLGSDPVLTPPNTVTLMGAEGRIITVGTSHPLYORGSSY 420
DB 361 PGRFGKRVQOAILSIKVSFSLGSDPVLTPPNTVTLMGAEGRIITVGTSHPLYORGSSY 420
QY 421 FSPALLYPMTVNKKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTYTDPYPLIFYR 480
DB 421 FSPALLYPMTVNKKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTYTDPYPLIFYR 480
QY 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSRITRVSSSTKAAVYTTSCFVKVTKNT 540
DB 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSRITRVSSSTKAAVYTTSCFVKVTKNT 540
QY 541 YCUSTIAEISNTLFGFRIVPLVLEILKNDGV 571
DB 541 YCUSTIAEISNTLFGFRIVPLVLEILKNDGV 571
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RESULT 15

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S40164
hemagglutinin-neuraminidase - Newcastle disease virus
C/Species: Newcastle disease virus
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C/Accession: S40164
R/Kallman, A.; Zadori, Z.; Kisari, J.; Podor, I.
submitted to the EMBL Data Library, May 1993
A/Description: Nucleotide sequence of the hemagglutinin-neuraminidase (HN) gene of newca
A/Reference number: S40163
A/Accession: S40164
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-571 <RAN>
A/Cross-references: EMBL:X71994; NID:9437888; PID:CA50868.1; PID:9437889
C/Superfamily: paramyxovirus hemagglutinin-neuraminidase
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Query Match 91.6%; Score 2746; DB 2; Length 571;
Best Local Similarity 90.7%; Pred. No. 2,1e-203;
Matches 518; Conservative 27; Mismatches 26; Indels 0; Gaps 0;
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QY 1 MDRASQVAVLENDREKNTWRLIFRIAILLTVVTLATSVASLVSMGASTPSDLVGP 60
DB 1 MDRASQVAVLENDREKNTWRLIFRIAILLTVVTLATSVASLVSMGASTPSDLVGP 60
QY 61 TRISRAEKTTSALGSQDVVDRIYKQVLESPLALNTEETIMNATLSYQINGAANN 120
DB 61 TRISRAEKTTSALGSQDVVDRIYKQVLESPLALNTEETIMNATLSYQINGAANN 120
QY 121 SGWCAPIHDDPFIIGIGKEILVDNASDVTSFYPSAFOEHLNFIAPATTGSGCTRIIPSDM 180
DB 121 SGWCAPIHDDPFIIGIGKEILVDNASDVTSFYPSAFOEHLNFIAPATTGSGCTRIIPSDM 180
QY 181 SATHYCYTANVILSGCRDHSHQYALGVLTATGRIFSTLRSISLDDTONRKSCSV 240
DB 181 SATHYCYTANVILSGCRDHSHQYALGVLTATGRIFSTLRSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKYTEETEEDYNASAVPTLMAHGRIGFQYHEKDLVTTLFEDWVANYP 300
DB 241 SATPLGCDMLCSKYTEETEEDYNASAVPTLMAHGRIGFQYHEKDLVTTLFEDWVANYP 300
QY 301 GVGGSFIDRWFVSYGGLKPNSPSDTVOEGKVYIKRYNDTCPPBODYQIIMAKSSYK 360
DB 301 GVGGSFIDRWFVSYGGLKPNSPSDTVOEGKVYIKRYNDTCPPBODYQIIMAKSSYK 360
QY 361 PGRFGKRVQOAILSIKVSFSLGSDPVLTPPNTVTLMGAEGRIITVGTSHPLYORGSSY 420
DB 361 PGRFGKRVQOAILSIKVSFSLGSDPVLTPPNTVTLMGAEGRIITVGTSHPLYORGSSY 420
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DB 361 PGRFGKRVQOAILSIKVSFSLGSDPVLTPPNTVTLMGAEGRIITVGTSHPLYORGSSY 420
QY 421 FSPALLYPMTVNKKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTYTDPYPLIFYR 480
DB 421 FSPALLYPMTVNKKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTYTDPYPLIFYR 480
QY 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSRITRVSSSTKAAVYTTSCFVKVTKNT 540
DB 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSRITRVSSSTKAAVYTTSCFVKVTKNT 540
QY 541 YCUSTIAEISNTLFGFRIVPLVLEILKNDGV 571
DB 541 YCUSTIAEISNTLFGFRIVPLVLEILKNDGV 571
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Search completed: January 2, 2004, 16:19:26
Job time : 30 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:51 / Search time 19 Seconds
(without alignments)
1428.127 Million cell updates/sec

Title: US-09-915-515A-1
Perfect score: 2998
Sequence: 1 MDRVSGVALENDERAKNT.....IVPLVLEILKNQGVREARSG 577

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt 41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2989	99.7	577 1 HEMA_NDV8	P32884 newcastle d
2	2938	98.0	577 1 HEMA_NDV8	P12553 newcastle d
3	2914	97.2	577 1 HEMA_NDV4	P12559 newcastle d
4	2913	97.2	577 1 HEMA_NDV1	P35743 newcastle d
5	2863	95.5	616 1 HEMA_NDV1	P12555 newcastle d
6	2862	95.5	616 1 HEMA_NDV1	P12558 newcastle d
7	2846	94.9	616 1 HEMA_NDV1	P13850 newcastle d
8	2763	92.2	571 1 HEMA_NDV3	P35741 newcastle d
9	2760	92.1	571 1 HEMA_NDV1	P12557 newcastle d
10	2758	92.0	571 1 HEMA_NDV1	P12554 newcastle d
11	2738.5	91.3	570 1 HEMA_NDV1	P12554 newcastle d
12	2711	90.4	571 1 HEMA_NDV1	P35740 newcastle d
13	2666	88.9	571 1 HEMA_NDV1	P35742 newcastle d
14	838	28.0	571 1 HEMA_NDV1	P25180 simian viru
15	781	26.1	582 1 HEMA_NDV1	P11235 mumps virus
16	778	26.0	571 1 HEMA_NDV1	P25466 human parai
17	777	25.9	571 1 HEMA_NDV1	P25465 human parai
18	772	25.8	565 1 HEMA_NDV1	P28885 simian viru
19	771	25.7	565 1 HEMA_NDV1	P28885 simian viru
20	770	25.7	582 1 HEMA_NDV1	P10866 mumps virus
21	765	25.5	565 1 HEMA_NDV1	P28883 simian viru
22	765	25.5	565 1 HEMA_NDV1	P28884 simian viru
23	759	25.3	582 1 HEMA_NDV1	P19762 mumps virus
24	689	23.0	573 1 HEMA_NDV1	P25526 human parai
25	480	16.0	575 1 HEMA_NDV1	P04853 sendai viru
26	479	16.0	575 1 HEMA_NDV1	P27562 sendai viru
27	479	16.0	575 1 HEMA_NDV1	P06863 sendai viru
28	469	15.6	575 1 HEMA_NDV1	P19758 sendai viru
29	455.5	15.2	572 1 HEMA_NDV1	P12556 human parai
30	448.5	15.0	576 1 HEMA_NDV1	P03425 human parai
31	445.5	14.9	572 1 HEMA_NDV1	P12562 human parai
32	444.5	14.8	572 1 HEMA_NDV1	P08492 human parai
33	444	14.8	572 1 HEMA_NDV1	P08492 human parai

34	441.5	14.7	572 1 HEMA_P13B	P06167 bovine para
35	441.5	14.7	572 1 HEMA_P13H	P12565 human parai
36	441	14.7	572 1 HEMA_P13H	P12564 human parai
37	439	14.6	572 1 HEMA_P13H	P12561 human parai
38	433.5	14.5	575 1 HEMA_P13H	P16071 human parai
39	145	4.8	1723 1 HEMA_P13H	P02812 chlamydia p
40	119	4.0	881 1 PRY3 YEAST	P47033 saccharomyc
41	118.5	4.0	5703 1 YN96 YEAST	P03684 homo sapien
42	112	3.7	1117 1 YN96 YEAST	P53753 saccharomyc
43	111.5	3.7	773 1 CDH PHACH	P01738 planerocoe
44	110	3.7	153 1 HEMA_MUMPS	P33480 mumps virus
45	109	3.6	670 1 YFGG_SCHPO	O13854 schizosacch

ALIGNMENTS

RESULT 1
HEMA_NDV8 STANDARD; PRT; 577 AA.
AC P32884; P06158;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN HN.
OS Newcastle disease virus (strain Beaudette C/45) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
OX NCBI_TaxID=11178;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66306666; PubMed=3018130;
RA Millar N.S., Chambers P., Emerson P.T.;
RT "Nucleotide sequence analysis of the haemagglutinin-neuraminidase
RT gene of Newcastle disease virus.";
RL J. Gen. Virol. 67:1917-1927(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89204897; PubMed=2705297;
RA Sakaguchi T., Toyoda T., Gotch B., Innocencio N.M., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. I. Multiple lineages defined by
RT sequence variability of the hemagglutinin-neuraminidase gene.";
RL Virology 169:260-272(1989).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC GLYCOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC N-TERMINAL HYDROPHOBIC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC NEURAMINIDASE FAMILY.
CC -----
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CC -----
CC EMBL: X04355; CA27880.1; -;
CC EMBL: M24710; AAA4660.1; -;
CC EMBL: A03663; CA00289.1; -;
CC PIR: F46328; F46328.
CC InterPro: IPR000665; Hem-neuramidase.
CC Pfam: PF00423; HN; 1.

KW Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;
 KM Tranmembrane.
 FT MOD RES 1 1 BLOCKED.
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 27 48 POTENTIAL.
 FT DOMAIN 49 577 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 577 AA; 63142 MW; 1D4C5284887EC1A1 CRC64;
 Query Match 99.7%; Score 2989; DB 1; Length 577;
 Best Local Similarity 99.7%; Pred. No. 8.5e-229;
 Matches 575; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDRASQVLENDERAKNTWRLIFRIALLLVTLATSVASLVSMGASTPSDVGIP 60
 DB 1 MDRASQVLENDERAKNTWRLIFRIALLLVTLATSVASLVSMGASTPSDVGIP 60
 QY 61 TRISRAEKTSLGSDVVDRIYQVVALESPALINTEITMNAITSLSQINGAANN 120
 DB 61 TRISRAEKTSLGSDVVDRIYQVVALESPALINTEITMNAITSLSQINGAANN 120
 QY 121 SGCGAPIHDPDFIGIGKELIVNADSVTSFYPSAQEHLNFIPTPTSGGCTRIIPSPDM 180
 DB 121 SGCGAPIHDPDFIGIGKELIVNADSVTSFYPSAQEHLNFIPTPTSGGCTRIIPSPDM 180
 QY 181 SATHYCYTHNVILSGCRDHS HQYALGVLTATGRIFFSTLRISLDDTONRKSCSV 240
 DB 181 SATHYCYTHNVILSGCRDHS HQYALGVLTATGRIFFSTLRISLDDTONRKSCSV 240
 QY 241 SATPLGCDMCSVYTEEDSDYNSAVPTLMAHRLGDDGQYHKDLDVTLTFEDWVANYP 300
 DB 241 SATPLGCDMCSVYTEEDSDYNSAVPTLMAHRLGDDGQYHKDLDVTLTFEDWVANYP 300
 QY 301 GVGGSFIDRWVPSYVGLKPNSPDPTVEGKVYIKRYNDTCPEBODYQIMAXSSYK 360
 DB 301 GVGGSFIDRWVPSYVGLKPNSPDPTVEGKVYIKRYNDTCPEBODYQIMAXSSYK 360
 QY 361 PGFRGKRIQOAILIKVSTSLGEDPVLTPPNTVTLMAGEGRLTVGTSHFLYORGSSY 420
 DB 361 PGFRGKRIQOAILIKVSTSLGEDPVLTPPNTVTLMAGEGRLTVGTSHFLYORGSSY 420
 QY 421 FSPALLYPMVSVKKTATLHSPYTNATFRGSI PCQASACPNSCVTGVYTDYPLIFR 480
 DB 421 FSPALLYPMVSVKKTATLHSPYTNATFRGSI PCQASACPNSCVTGVYTDYPLIFR 480
 QY 481 NHTLRGVFGTMDSEQARLNPAFSDTSRSRTTRVSSSTAAAYTTSTCFKVVTKNTK 540
 DB 481 NHTLRGVFGTMDSEQARLNPAFSDTSRSRTTRVSSSTAAAYTTSTCFKVVTKNTK 540
 QY 541 YCLSIATISNTLFGFEFRIPLVLEILKNDGVREARSG 577
 DB 541 YCLSIATISNTLFGFEFRIPLVLEILKNDGVREARSG 577
 RESULT 2
 HEMA_NDVVG STANDARD; PRT; 577 AA.
 AC P12553;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
 GN HN.
 OS Newcastle disease virus (strain Texas G.b./48) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae;
 OC NCBI_TaxID=11189;
 OC [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=88265873; PubMed=3388773;
 RA Schaper U.M., Fuller F.J., Ward M.D.W., Mehrotra Y., Stone H.O.,
 RA Stripp B.R., de Buyscher E.V.;
 RT "Nucleotide sequence of the envelope protein genes of a highly
 RT virulent, neurotropic strain of Newcastle disease virus."
 RL Virology 165:251-295(1988).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204897; PubMed=2705297;
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,
 RA Nagai Y.;
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by
 RT sequence variability of the hemagglutinin-neuraminidase gene."
 RL Virology 169:260-272(1989).
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
 CC GLYCOPROTEINS.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
 CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
 CC NEURAMINIDASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M21409; AAA4669.1; -
 DR EMBL; M24711; AAA4661.1; -
 DR InterPro: IPR000665; Hem-neuraminidase.
 DR Pfam: PF00423; HN.1
 KW Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;
 KM Tranmembrane.
 FT MOD RES 1 1 BLOCKED.
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 27 48 POTENTIAL.
 FT DOMAIN 49 577 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 160 H -> L (IN REF. 2).
 FT CONFLICT 332 E -> R (IN REF. 2).
 SQ SEQUENCE 577 AA; 63275 MW; 75CC2A5255626140 CRC64;
 Query Match 98.0%; Score 2938; DB 1; Length 577;
 Best Local Similarity 97.9%; Pred. No. 9.2e-225;
 Matches 565; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MDRASQVLENDERAKNTWRLIFRIALLLVTLATSVASLVSMGASTPSDVGIP 60
 DB 1 MDRASQVLENDERAKNTWRLIFRIALLLVTLATSVASLVSMGASTPSDVGIP 60
 QY 61 TRISRAEKTSLGSDVVDRIYQVVALESPALINTEITMNAITSLSQINGAANN 120
 DB 61 TRISRAEKTSLGSDVVDRIYQVVALESPALINTEITMNAITSLSQINGAANN 120
 QY 121 SGCGAPIHDPDFIGIGKELIVNADSVTSFYPSAQEHLNFIPTPTSGGCTRIIPSPDM 180
 DB 121 SGCGAPIHDPDFIGIGKELIVNADSVTSFYPSAQEHLNFIPTPTSGGCTRIIPSPDM 180
 QY 181 SATHYCYTHNVILSGCRDHS HQYALGVLTATGRIFFSTLRISLDDTONRKSCSV 240
 DB 181 SATHYCYTHNVILSGCRDHS HQYALGVLTATGRIFFSTLRISLDDTONRKSCSV 240


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QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVANYP 300
DB 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVANYP 300
QY 301 GVGGSFIDGRVWPSVYGLKPNPSDPTVOEGKVIYKRYNDTCDEDDYQIRAKSSYK 360
DB 301 GVGGSFIDGRVWPSVYGLKPNPSDPTVOEGKVIYKRYNDTCDEDDYQIRAKSSYK 360
QY 361 PGRFGKRIQQAILISIKVTSISGDEPVLTPPNTVTLMGAGRILTVGTSHPLYORSSY 420
DB 361 PGRFGKRIQQAILISIKVTSISGDEPVLTPPNTVTLMGAGRILTVGTSHPLYORSSY 420
QY 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVYTDPPYLFYR 480
DB 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVYTDPPYLFYR 480
QY 481 NHTLRGVGTMLDGOARLNPASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKNT 540
DB 481 NHTLRGVGTMLDGOARLNPASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKNT 540
QY 541 YCLSIASISNTLFGFRIPLVPLVEILKNDGVREARSG 577
DB 541 YCLSIASISNTLFGFRIPLVPLVEILKNDGVREARSG 577

RESULT 3
HEMA_NDVH4 STANDARD; PRT; 577 AA.
AC P12559; P06158;
DT 01-OCT-1989, (Rel. 12, Created)
DT 01-OCT-1989, (Rel. 12, Last sequence update)
DT 16-OCT-2001, (Rel. 40, Last annotation update)
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN HN.
OS Newcastle disease virus (strain BI-Hitchner/47) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.
OX NCBI_Taxid=11181;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3027962;
RX MEDLINE=87122141;
RA Jorgensen E.D., Collins P.L., Lomedico P.T.;
RT "Cloning and nucleotide sequence of Newcastle disease virus hemagglutinin-neuraminidase mRNA: identification of a putative sialic acid binding site."
RT Virology 156:12-24(1987).
RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=89204897; PubMed=2705297;
RX Sakaguchi T., Toyoda T., Gotch B., Innocencio N.M., Kuma K., Miyata T., Nagai Y.;
RT "Newcastle disease virus evolution. I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene."
RT Virology 169:260-272(1989).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING GLYCOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS N-TERMINAL HYDROPHOBIC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-NEURAMINIDASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M16573; AAA46668.1; -.
DR EMBL; M24708; AAA46658.1; -.
DR PIR; A26355; HNNZNC.
DR InterPro; IPR000665; Hem-neuramndase.
DR Pfam; PF00423; HN; 1.
KW Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;
KW Transmembrane.
FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 27 48 POTENTIAL.
FT DOMAIN 49 577 EXTRACELLULAR (POTENTIAL).
FT CARBOHD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 200 200 L -> S (IN REF. 2).
FT CONFLICT 203 203 L -> Y (IN REF. 2).
FT CONFLICT 324 324 T -> S (IN REF. 2).
SQ SEQUENCE 577 AA; 63241 MW; A7BCF780A8FF70E CRC64;

Query Match 97.2%; Score 2914; DB 1; Length 577;
Best Local Similarity 96.7%; Pred. No. 7,3e-223;
Matches 558; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDRVSOVALENDERREAKNTWRLIFRIALLITVVTATSVASLYVSGASTPSDLVGP 60
DB 1 MDRVSOVALENDERREAKNTWRLIFRIALLITVVTATSVASLYVSGASTPSDLVGP 60
QY 61 TRIRAEKITSATGSDNODVDRIYKOVALESPLALNTETTNNATSTLSYOINGANN 120
DB 61 TRIRAEKITSATGSDNODVDRIYKOVALESPLALNTETTNNATSTLSYOINGANN 120
QY 121 SGMGAPIDPDPIGIGIKELIVDNASDVTSPYPAFOHNFIPAPTTGSGCTRIPSFDM 180
DB 121 SGMGAPIDPDPIGIGIKELIVDNASDVTSPYPAFOHNFIPAPTTGSGCTRIPSFDM 180
QY 181 SATYCYTHNVILSGCRDHSHOYLALGVLRRTATGRIFPSTLRSLDPTONRKSCSV 240
DB 181 SATYCYTHNVILSGCRDHSHOYLALGVLRRTATGRIFPSTLRSLDPTONRKSCSV 240
QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVANYP 300
DB 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVANYP 300
QY 301 GVGGSFIDGRVWPSVYGLKPNPSDPTVOEGKVIYKRYNDTCDEDDYQIRAKSSYK 360
DB 301 GVGGSFIDGRVWPSVYGLKPNPSDPTVOEGKVIYKRYNDTCDEDDYQIRAKSSYK 360
QY 361 PGRFGKRIQQAILISIKVTSISGDEPVLTPPNTVTLMGAGRILTVGTSHPLYORSSY 420
DB 361 PGRFGKRIQQAILISIKVTSISGDEPVLTPPNTVTLMGAGRILTVGTSHPLYORSSY 420
QY 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVYTDPPYLFYR 480
DB 421 FSPALLYPMVTSNKTATLHSPYTNAFTFRPGSIPCOASARCPNSCVTVYTDPPYLFYR 480
QY 481 NHTLRGVGTMLDGOARLNPASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKNT 540
DB 481 NHTLRGVGTMLDGOARLNPASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKNT 540
QY 541 YCLSIASISNTLFGFRIPLVPLVEILKNDGVREARSG 577
DB 541 YCLSIASISNTLFGFRIPLVPLVEILKNDGVREARSG 577

RESULT 4
HEMA_NDVH4 STANDARD; PRT; 577 AA.
AC P35743;
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DR EMBL; M19432; AAA46638.1; -;
 DR EMBL; M24705; AAA46655.1; -;
 DR PIR; A46328; A46328.
 DR InterPro; IPR000665; Hem-neuramidase.

DR Pfam; PF00423; HN; 1.
 KM Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;
 Transmembrane.

FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 27 48 POTENTIAL.
 FT DOMAIN 49 616 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 199 199 R -> H (IN REF. 2).
 SQ SEQUENCE 616 AA; 67680 MW; 2PDE7785C5DA62AA CRC64;

Query Match 95.5%; Score 2863; DB 1; Length 616;
 Best Local Similarity 94.5%; Pred. No. 8.7e-219;
 Matches 545; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDRVAVSVALENDREKAKNTWRLIFRIALLITVTLATSVASLVSGASTPSDLVGP 60
 DB 1 MDRVAVSVALENDREKAKNTWRLIFRIALLITVTLATSVASLVSGASTPSDLVGP 60
 QY 61 TRISRAEKTISALGSNOVDVDRIRYKVALSPALANTETTMMATISLSTQINGAAN 120
 DB 61 TRISRAEKTISALGSNOVDVDRIRYKVALSPALANTETTMMATISLSTQINGAAN 120
 QY 121 SGMCAPIHDPDIFGIGKELIVNADSVTSFYPSPFOEHLNIFAPPTGSGCTRIPSPDM 180
 DB 121 SGMCAPIHDPDIFGIGKELIVNADSVTSFYPSPFOEHLNIFAPPTGSGCTRIPSPDM 180
 QY 181 SATHYCYTHNVILSGCRDHSHQYLAAGVLTATGRIFFSTLRSLSDDTQNRKCSV 240
 DB 181 SATHYCYTHNVILSGCRDHSHQYLAAGVLTATGRIFFSTLRSLSDDTQNRKCSV 240
 QY 241 SATPLGCDMLCSKTEETBEDYNSAVPLTMAHGRGFGQYHEKDLDTTLFEDMVANYP 300
 DB 241 SATPLGCDMLCSKTEETBEDYNSAVPLTMAHGRGFGQYHEKDLDTTLFEDMVANYP 300
 QY 301 GVGGSPIIDGRVWVSVYGLKPNSPDVTGEGKVYIKRVNDTPDDODVDIRAKSSYK 360
 DB 301 GVGGSPIIDGRVWVSVYGLKPNSPDVTGEGKVYIKRVNDTPDDODVDIRAKSSYK 360
 QY 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPVNTVTLMAAGRIITVGTSHFLYQSSSY 420
 DB 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPVNTVTLMAAGRIITVGTSHFLYQSSSY 420
 QY 421 FSPALLIPMTVSNKTATLHSPYTNAFTPGSIFCOASARCPNSCVTGYTDPYPLFYR 480
 DB 421 FSPALLIPMTVSNKTATLHSPYTNAFTPGSIFCOASARCPNSCVTGYTDPYPLFYR 480
 QY 481 NHTLRGVGTMDEQARLNPAVFPDSTSRITRVSSTSKAAYTSCTCFKVKTKNT 540
 DB 481 NHTLRGVGTMDEQARLNPAVFPDSTSRITRVSSTSKAAYTSCTCFKVKTKNT 540
 QY 541 YCLSIABISNTLFGFRIIVPLVLEILKNDGVREARSG 577
 DB 541 YCLSIABISNTLFGFRIIVPLVLEILKNDGVREARSG 577

RESULT 6
 HEMA_NDVU

ID HEMA_NDVU STANDARD; PRT; 616 AA.
 AC P12558;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18)..
 GN HN.
 OS Newcastle disease virus (strain Ulster/67) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
 CX NCBI_TaxId=11190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88174450; PubMed=3351479;
 RA Millar N.S., Chambers P., Emerson P.T.;
 RT "Nucleotide sequence of the fusion and haemagglutinin-neuraminidase
 RT glycoprotein genes of Newcastle disease virus, strain Ulster;
 RT molecular basis for variations in pathogenicity between strains."
 RN J. Gen. Virol. 69:613-620(1988).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88160043; PubMed=2450424;
 RA Gotoh B., Sakaguchi T., Nishikawa K., Innocencio N.M., Hamaguchi M.,
 RA Toyoda T., Nagai Y.;
 RT "Structural features unique to each of the three antigenic sites on
 RT the hemagglutinin-neuraminidase protein of Newcastle disease virus."
 RL Virology 163:174-182(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204897; PubMed=2705297;
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,
 RA Nagai Y.;
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by
 RT sequence variability of the hemagglutinin-neuraminidase gene."
 RL Virology 163:260-272(1989).
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
 CC GLYCOPROTEINS.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
 CC NEURAMINIDASE FAMILY.
 CC
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DR EMBL; D00243; BAA00174.1; -;
 DR EMBL; M19478; AAA46677.1; -;
 DR EMBL; M24707; AAA46657.1; -;
 DR EMBL; A03672; CAA00292.1; -;
 DR PIR; B29823; HNNZU1.
 DR PIR; C46328; C46328.
 DR InterPro; IPR000665; Hem-neuramidase.
 DR Pfam; PF00423; HN; 1.
 KM Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;
 Transmembrane.
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 27 48 POTENTIAL.
 FT DOMAIN 49 616 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 74 74 L -> S (IN REF. 2).
 FT CONFLICT 74 74 L -> H (IN REF. 3).
 FT CONFLICT 259 259 E -> K (IN REF. 2).
 FT CONFLICT 438 438 L -> R (IN REF. 2).
 FT CONFLICT 495 495 K -> E (IN REF. 2).
 FT CONFLICT 555 555 EF -> GI (IN REF. 3).
 SQ SEQUENCE 616 AA: 67590 MW: E70D67796FDD3A36 CRC64;

Query Match 95.5%; Score 2862; DB 1; Length 616;
 Best Local Similarity 94.3%; Pred. No. 1e-217;

Matches 544; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 1 MDRASQVLENDEREAKNTWRIIFRIALLTVVTATSVASLVYSGASTPSDVGIP 60
 DB 1 MDRASQVLENDEREAKNTWRIIFRIALLTVVTATSAALAVSMASSTPSDVGIP 60
 QY 61 TRISRAEEKITSAAGSNQDVVDRIYKQVALESPLALNTETTIMAITSLSYQINGAANN 120
 DB 61 TRISRAEEKITSAAGSNQDVVDRIYKQVALESPLALNTETTIMAITSLSYQINGAANS 120
 QY 121 SGHGAPIHDPDFTGGIGKEILVDNASDVTSFYPSAFQEHINFIAPPTGSGCTRIIPSPDM 180
 DB 121 SGCGAPIHDPDFTGGIGKEILVDNASDVTSFYPSAFQEHINFIAPPTGSGCTRIIPSPDM 180
 QY 181 SAHYCTTHNVIIISGCDHSHSHOYLALGYLRTATCRIFSTLRSLDDTONRSCSV 240
 DB 181 SAHYCTTHNVIIISGCDHSHSHOYLALGYLRTATCRIFSTLRSLDDTONRSCSV 240
 QY 241 SATPLGCDMLCSKTEEREDYNSAVPTLMAHGLGPDGYHEKDLDTTLTFEDWVANY 300
 DB 241 SATPLGCDMLCSKTEEREDYNSAVPTLMAHGLGPDGYHEKDLDTTLTFEDWVANY 300
 QY 301 GVGGSFIDGRWVPSVYGGKPNSSDTVQEGKVIYKRYNDTCPEBDYQIIMAKSSYK 360
 DB 301 GVGGSFIDGRWVPSVYGGKPNSSDTVQEGKVIYKRYNDTCPEBDYQIIMAKSSYK 360
 QY 361 PGRFGGRIGQIALISTVSTSLGSDPVLTPPMTVTLMAGEGVLTGVTSHPLYOGSSY 420
 DB 361 PGRFGGRIGQIALISTVSTSLGSDPVLTPPMTVTLMAGEGVLTGVTSHPLYOGSSY 420
 QY 421 FSPALLYPMVSNKATLHSPYTFENAFTRPGSIIPCOASACPNSCVTGYTDPYPLIFR 480
 DB 421 FSPALLYPMVSNKATLHSPYTFENAFTRPGSIIPCOASACPNSCVTGYTDPYPLIFR 480
 QY 481 NHTLRGVFGTMDLSEQARLNPASAVFSDTSRSRTTRVSSSTRAAYTTSTCFKVVKTNT 540
 DB 481 NHTLRGVFGTMDLSEQARLNPASAVFSDTSRSRTTRVSSSTRAAYTTSTCFKVVKTNT 540
 QY 541 YCISIAEISNTLFGEPRIYVPLVILKNDGVRARSG 577
 DB 541 YCISIAEISNTLFGEPRIYVPLVILKNDGVRARSG 577

RESULT 7

HEMA_NDVQ STANDARD; PRT; 616 AA.

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
 GN HN.
 OS Newcastle disease virus (strain Queensland/66) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Monomsgavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae;
 OC NCBI_Taxid=11166;

RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=88315049; Pubmed=3045120;
 RA Gorman J.J., Nestorowicz A., Mitchell S.J., Corino G.L., Sellsack P.W.;

RT "Characterization of the sites of proteolytic activation of Newcastle
 RT disease virus membrane glycoprotein precursors";
 RL J. Biol. Chem. 263:12523-12531(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204897; Pubmed=2705297;
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,
 RA Nagai Y.;
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by
 RT sequence variability of the hemagglutinin-neuraminidase gene";
 RL Virology, 169:260-272(1989).
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
 CC GLYCOPROTEINS.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
 CC NEURAMINIDASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: J03911; AAA46554.1; -
 DR EMBL: M24706; AAA46556.1; -
 DR PIR: A31110; HNNZQD.
 DR PIR: B46328; B46328.
 DR InterPro: IPR000665; Hem-neuramidae.
 DR Pfam: PF00423; HN; 1.
 KW Hydrolaase, Hemagglutinin, Envelope protein; Glycoprotein;
 KW Transmembrane.
 FT DOMAIN 1 26
 FT TRANSMEM 27 48
 FT POTENTIAL.
 FT DOMAIN 49 616
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 87 87 O -> H (IN REF. 2).
 FT CONFLICT 113 113 R -> Q (IN REF. 2).
 FT CONFLICT 151 151 Y -> F (IN REF. 2).
 FT CONFLICT 432 432 S -> G (IN REF. 2).
 FT CONFLICT 495 495 K -> E (IN REF. 2).
 SQ SEQUENCE 616 AA: 67656 MW: CBF556EB3B8C60F CRC64;

Query Match 94.9%; Score 2846; DB 1; Length 616;

Best Local Similarity 93.9%; Pred. No. 1.9e-217; Indels 0; Gaps 0;

Matches 541; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 MDRASQVLENDEREAKNTWRIIFRIALLTVVTATSVASLVYSGASTPSDVGIP 60
 DB 1 MDRASQVLENDEREAKNTWRIIFRIALLTVVTATSAALAVSMASSTPSDVGIP 60
 QY 61 TRISRAEEKITSAAGSNQDVVDRIYKQVALESPLALNTETTIMAITSLSYQINGAANN 120
 DB 61 TRISRAEEKITSAAGSNQDVVDRIYKQVALESPLALNTETTIMAITSLSYQINGAANS 120
 QY 121 SGHGAPIHDPDFTGGIGKEILVDNASDVTSFYPSAFQEHINFIAPPTGSGCTRIIPSPDM 180
 DB 121 SGCGAPIHDPDFTGGIGKEILVDNASDVTSFYPSAFQEHINFIAPPTGSGCTRIIPSPDM 180

QY 181 SATHYCTHNVITLSCGRDHSQYLAAGVLTATGRIFFSTLRISLDTONKSCSV 240
 Db 181 SATHYCTHNVITLSCGRDHSQYLAAGVLTATGRIFFSTLRISLDTONKSCSV 240
 QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFGQYHEKDLDVTLTPEDMVANYP 300
 Db 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFGQYHEKDLDVTLTPEDMVANYP 300
 QY 301 GVGGGSPFDGRWVSVYGLKPNPSPTVOEGKYIYKRYNDTCPEDDOYQIRMAKSSYK 360
 Db 301 GVGGGSPFDGRWVSVYGLKPNPSPTVOEGKYIYKRYNDTCPEDDOYQIRMAKSSYK 360
 QY 361 PGRFGKRIQOALISIKVSTSLGEDPVLTVPNTVTLMGAEGRLITVGTSHFLYQSGSSY 420
 Db 361 PGRFGKRIQOALISIKVSTSLGEDPVLTVPNTVTLMGAEGRLITVGTSHFLYQSGSSY 420
 QY 421 FSPALLVPMYVSNKATLHSPYTFNAFTPRPSIPCOASARCPNSCVTVTDPPPLIYR 480
 Db 421 FSPALLVPMYVSNKATLHSPYTFNAFTPRPSIPCOASARCPNSCVTVTDPPPLIYR 480
 QY 481 NHTLRGVGTMLDSEQARLNPAASAVFDSTSRRTIRVSSSTKAAVTTSTGPKVVKTKTKT 540
 Db 481 NHTLRGVGTMLDSEQARLNPAASAVFDSTSRRTIRVSSSTKAAVTTSTGPKVVKTKTKT 540
 QY 541 YCLSIATISNTLFGFRIPLVPLVLEILKNDGVREARS 576
 Db 541 YCLSIATISNTLFGFRIPLVPLVLEILKNDGVREARS 576

RESULT 8

HEMA_NDVH3 STANDARD; PRT; 571 AA.

AC P15741;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
 GN HN.
 OS Newcastle disease virus (strain Her/33) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
 OC NCBI_TaxID=1187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204897; PubMed=2705297;
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,
 Nagai Y.;
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by
 RT sequence variability of the hemagglutinin-neuraminidase gene."; *Virology* 169:260-272(1989).
 RL -1- PUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
 TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
 ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
 THE NATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
 GLYCOPROTEINS.
 -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 oligosaccharides, glycoproteins, glycolipids, colominic acid and
 synthetic substrates.
 CC SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
 CC NEURAMINIDASE FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC EMBL; M24714; AAA46664.1; -

DR PIR; A36829.
 DR InterPro; IPR000665; Hem-neuramndse.
 DR Pfam; PF00423; HN; 1.
 KW Hydroxylase; Hemagglutinin; Envelope protein; Glycoprotein;
 KW Transmembrane.
 FT DOMAIN 1 26
 FT TRANSMEM 27 48
 FT DOMAIN 49 571
 FT CARBOHYD 119 119
 FT CARBOHYD 341 341
 FT CARBOHYD 433 433
 FT CARBOHYD 481 481
 FT CARBOHYD 508 508
 FT CARBOHYD 538 538
 SQ SEQUENCE 571 AA; 62609 MW; 60EB6A508C8A1BF CRC64;

Query Match 92.2%; Score 2763; DB 1; Length 571;
 Best Local Similarity 91.6%; Pred. No. 6.5e-211;
 Matches 523; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDRVSOVLENDERBAKNTWRLFIATLITVTLATSVASIVMGASTPDLVIGIP 60
 Db 1 MDRVSRVLENDERBAKNTWRFVRIATLITVTLATSVASIVMGASTPDLVIGIP 60
 QY 61 TRIGRAEKITSALGSNOVDVDRITYKOVLESPLALINTETITNNATISLVSQINGAANN 120
 Db 61 TVIRAEKITSALSNQDVDRITYKOVLESPLALINTESVIMNATISLVSQINGAANN 120
 QY 121 SGWAPLHDPDFIGIGELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
 Db 121 SGCGAPYHDPYIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
 QY 181 SATHYCTHNVITLSCGRDHSQYLAAGVLTATGRIFFSTLRISLDTONKSCSV 240
 Db 181 SATHYCTHNVITLSCGRDHSQYLAAGVLTATGRIFFSTLRISLDTONKSCSV 240
 QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFGQYHEKDLDVTLTPEDMVANYP 300
 Db 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFGQYHEKDLDVTLTPEDMVANYP 300
 QY 301 GVGGGSPFDGRWVSVYGLKPNPSPTVOEGKYIYKRYNDTCPEDDOYQIRMAKSSYK 360
 Db 301 GVGGGSPFDGRWVSVYGLKPNPSPTVOEGKYIYKRYNDTCPEDDOYQIRMAKSSYK 360
 QY 361 PGRFGKRIQOALISIKVSTSLGEDPVLTVPNTVTLMGAEGRLITVGTSHFLYQSGSSY 420
 Db 361 PGRFGKRIQOALISIKVSTSLGEDPVLTVPNTVTLMGAEGRLITVGTSHFLYQSGSSY 420
 QY 421 FSPALLVPMYVSNKATLHSPYTFNAFTPRPSIPCOASARCPNSCVTVTDPPPLIYR 480
 Db 421 FSPALLVPMYVSNKATLHSPYTFNAFTPRPSIPCOASARCPNSCVTVTDPPPLIYR 480
 QY 481 NHTLRGVGTMLDSEQARLNPAASAVFDSTSRRTIRVSSSTKAAVTTSTGPKVVKTKTKT 540
 Db 481 NHTLRGVGTMLDSEQARLNPAASAVFDSTSRRTIRVSSSTKAAVTTSTGPKVVKTKTKT 540
 QY 541 YCLSIATISNTLFGFRIPLVPLVLEILKNDGV 571
 Db 541 YCLSIATISNTLFGFRIPLVPLVLEILKNDGV 571

RESULT 9

HEMA_NDVH3 STANDARD; PRT; 571 AA.

AC P12557;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
 GN HN.
 OS Newcastle disease virus (strain Miyadera/51) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.

NCBI_TaxID=11185;
 (1) SEQUENCE FROM N.A.
 RX MEDLINE=86160043; Pubmed=2450424;
 RA Gotoh B., Sakaguchi T., Nishikawa K., Innocencio N.M., Hamaguchi M.,
 Toyoda T., Nagai Y.;
 RT "Structural features unique to each of the three antigenic sites on
 the hemagglutinin-neuraminidase protein of Newcastle disease virus";
 Virology 163:174-182(1988).
 (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204897; Pubmed=2705297;
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,
 Nagai Y.;
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by
 sequence variability of the hemagglutinin-neuraminidase gene";
 Virology 163:260-272(1989).
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
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 oligosaccharides, glycoproteins, glycolipids, colominic acid and
 synthetic substrates.
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
 N-TERMINAL HYDROPHOBIC SEQUENCE.
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
 NEURAMINIDASE FAMILY.
 CC -----
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 or send an email to license@1sb-sib.ch).
 CC -----
 DR EMBL; M19479; AAA46674.1; -;
 DR EMBL; M24713; AAA46663.1; -;
 DR InterPro; IPR000665; Hem-neuramidase.
 DR Pfam; PF00423; HN; 1.
 KM Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;
 KM Transmembrane.
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 27 48 POTENTIAL.
 FT DOMAIN 49 571 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 167 167 T -> P (IN REF. 2).
 SQ SEQUENCE 571 AA; 62522 MW; F2891CE5137937D5 CRC64;
 Query Match 92.1%; Score 2760; DB 1; Length 571;
 Best Local Similarity 91.6%; Pred. No. 1,le-210;
 Matches 523; Conservative 22; Mismatches 26; Indels 0; Gaps 0;
 QY 1 MDRVAVOALVENEERAKNTWRLIFRIALLTVTLATVASIVVSMGASTSDLVGIP 60
 DB 1 MDRVAVOALVENEERAKNTWRLIFRIALLTVTLATVASIVVSMGASTSDLVGIP 60
 QY 61 TRISRAEKTISALGSNOVDVRIKVOALESPLALNTEETIMATISLSTYINGANN 120
 DB 61 TRISRAEKTISALGSNOVDVRIKVOALESPLALNTEETIMATISLSTYINGANN 120
 QY 121 SGNGAPRHDDDFIGIGIKELIVDNASDVTSFYSAPFENLNPAPPTGSGCCTRI9SFD 180
 DB 121 SGNGAPRHDDDFIGIGIKELIVDNASDVTSFYSAPFENLNPAPPTGSGCCTRI9SFD 180
 QY 121 SGNGAPRHDDDFIGIGIKELIVDNASDVTSFYSAPFENLNPAPPTGSGCCTRI9SFD 180
 DB 121 SGNGAPRHDDDFIGIGIKELIVDNASDVTSFYSAPFENLNPAPPTGSGCCTRI9SFD 180

QY 181 SATHVCTYHNVLISGCRDHSQVYALGVLTATGRIFPSTLRSISLDDTQNRKSCSV 240
 DB 181 SATHVCTYHNVLISGCRDHSQVYALGVLTATGRIFPSTLRSISLDDTQNRKSCSV 240
 QY 241 SATPLCCDMLCSKVTEEBEDYNNAVITLMANGRLGFCQYHEKLDVTTLEEDVYANP 300
 DB 241 SATPLCCDMLCSKVTEEBEDYNNAVITLMANGRLGFCQYHEKLDVTTLEEDVYANP 300
 QY 301 GVGGSFFIDGRWFSVYGGALKPNSPEDTVOEGEKVYIKKYNTPCEPDQYQIRMAKSSYK 360
 DB 301 GVGGSFFIDGRWFSVYGGALKPNSPEDTVOEGEKVYIKKYNTPCEPDQYQIRMAKSSYK 360
 QY 361 PGRFGKRIQOAILSIKYSTSLGEBDVLTPPNTVTLMGAEGRILVTGSHFLYGRSSY 420
 DB 361 PGRFGKRIQOAILSIKYSTSLGEBDVLTPPNTVTLMGAEGRILVTGSHFLYGRSSY 420
 QY 421 FSPALLYPTVSNKRTATLHSPYTFNAFTTPGSLPCQASARCNSCYTYTDPYPLIFR 480
 DB 421 FSPALLYPTVSNKRTATLHSPYTFNAFTTPGSLPCQASARCNSCYTYTDPYPLIFR 480
 QY 481 NHTLRGVFGTMDSEQRALNPASAVDSRSRITPVSSTTKAAYTSTCFKVKVTKNT 540
 DB 481 NHTLRGVFGTMDSEQRALNPASAVDSRSRITPVSSTTKAAYTSTCFKVKVTKNT 540
 QY 541 YCLSIATISNTLFGERRIVPLVLEIKNDGV 571
 DB 541 YCLSIATISNTLFGERRIVPLVLEIKNDGV 571
 RESULT 10
 ID HEMA NDVI STANDARD; PRT; 571 AA.
 AC P12556;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
 GN HN.
 OS Newcastle disease virus (strain Italien/45) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.
 OX NCBI_TaxID=11182;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88076411; Pubmed=3318761;
 RA Memets C.D., de Henau S., Neyt C., Espion D., Letellier C.,
 Meulemans G., Bury A.;
 RT "The hemagglutinin-neuraminidase (HN) gene of Newcastle disease virus
 strain Italien (NDV Italien): comparison with HNs of other strains
 and expression by a vaccinia recombinant.";
 RL Arch. Virol. 97:101-113(1987).
 (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204897; Pubmed=2705297;
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,
 Nagai Y.;
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by
 sequence variability of the hemagglutinin-neuraminidase gene";
 Virology 163:260-272(1989).
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
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 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 oligosaccharides, glycoproteins, glycolipids, colominic acid and
 synthetic substrates.
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
 N-TERMINAL HYDROPHOBIC SEQUENCE.
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
 NEURAMINIDASE FAMILY.
 CC -----

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DR EMBL; M18640; AAA46671.1; -
 DR EMBL; M24715; AAA46665.1; -
 DR PIR; S07126; B36829
 DR InterPro; IPR000655; Hem-neuramndse.
 DR Pfam; PF00423; HN; 1.
 KW Hydroxylase; Hemagglutinin; Envelope protein; Glycoprotein;
 KW Transmembrane.
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 27 48 POTENTIAL.
 FT DOMAIN 49 571 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 3 4 RA -> LP (IN REF. 2).
 FT CONFLICT 52 52 T -> S (IN REF. 2).
 FT CONFLICT 75 75 S -> G (IN REF. 2).
 FT CONFLICT 216 216 T -> A (IN REF. 2).
 FT CONFLICT 400 401 PE -> AD (IN REF. 2).
 FT SEQUENCE 571 AA; 62604 MW; F1ECB12BEF46C00F CRC64;

Query Match 92.0%; Score 2758; DB 1; Length 571;
 Best Local Similarity 91.1%; Pred. No. 1.6e-210;
 Matches 520; Conservative 25; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDRASQVALENDEREAKNTWRLIRIAILLITVTATSVASLVYSGASTPSDLVGIP 60
 DB 1 MDRAGRAVALENEEREAQNTWRFRIALFLITVITLISAALVYSGASTPSDLVGIP 60
 QY 61 TRISAEEKITSAAGSNODVDRIYKOVALBESPLALMTETITMAAISLSQINGANN 120
 DB 61 TVISAEEKITSAAGSNODVDRIYKOVALBESPLALMTETITMAAISLSQINGANN 120
 QY 121 SGWGPADHPDPIGIGELIYDNASDVTSFYPASFOEHLNIPAPPTGSGGCTRIPSFDM 180
 DB 121 SGCGAPVADPDVIGIGELIYDSDVTSFYPASFOEHLNIPAPPTGSGGCTRIPSFDM 180
 QY 181 SATHYCYTHNVILSGCRDHSHQYLAGVLTATGRI PFSTLRSISLDDTONKSCSV 240
 DB 181 SATHYCYTHNVILSGCRDHSHQYLAGVLTATGRI PFSTLRSISLDDTONKSCSV 240
 QY 241 SATPLGCMGSKVTEDEEDNSAVPTLMAGRLGPGQCHERKLDVTLPEDEVANYP 300
 DB 241 SATPLGCMGSKVTEDEEDNSAVPTLMAGRLGPGQCHERKLDVTLPEDEVANYP 300
 QY 301 GVGGGSFIDGRVWFVYGLKPNSPDVYOEKGYIYKRYNDTCDEDOYQIRMAKSSYK 360
 DB 301 GVGGGSFIDGRVWFVYGLKPNSPDVYOEKGYIYKRYNDTCDEDOYQIRMAKSSYK 360
 QY 361 GVGGSFIDNRVWFVYGLKPNSSDPAQEKRYIYKRYNDTCDEDOYQIRMAKSSYK 360
 DB 361 GVGGSFIDNRVWFVYGLKPNSSDPAQEKRYIYKRYNDTCDEDOYQIRMAKSSYK 360
 QY 420 361 GVRFGSKRIQQAIIISIKVTSIGEDPVLTPPNTVTLMGAGRIITVGTSHLYRGSSY 420
 DB 420 361 GVRFGSKRIQQAIIISIKVTSIGEDPVLTPPNTVTLMGAGRIITVGTSHLYRGSSY 420
 QY 480 421 FSPALYPMYTSNKATLHSPPTFAAFTRPGSIPCOASARCNSCVTVYDPPYLYR 480
 DB 480 421 FSPALYPMYTSNKATLHSPPTFAAFTRPGSIPCOASARCNSCVTVYDPPYLYR 480
 QY 540 481 NHTLKGVTGTMDSQARLNPAFAVFDSTSRIRTRVSSSTKAYATTSTCKVYKTKT 540
 DB 540 481 NHTLKGVTGTMDSQARLNPAFAVFDSTSRIRTRVSSSTKAYATTSTCKVYKTKT 540
 QY 541 YCLSTIAEISNTLFGFRIVPLLVLEILKNDGV 571
 DB 541 YCLSTIAEISNTLFGFRIVPLLVLEILKNDGV 571

DB 541 YCLSTIAEISNTLFGFRIVPLLVLEILKNDGV 571
 RESULT 11
 HEMA_NDVA
 ID_HEMA_NDVA STANDARD; PRT; 570 AA.
 AC P12554;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
 GN HN.
 OS Newcastle disease virus (strain Australia-Victoria/32) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 OX NCBI_TaxID=11177;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87266149; PubMed=3037818;
 RA McGlimes L.W., Wilde A., Morrison T.G.;
 RT "Nucleotide sequence of the gene encoding the Newcastle disease virus hemagglutinin-neuraminidase protein and comparisons of paramyxovirus hemagglutinin-neuraminidase protein sequences.";
 RL Virus Res. 7:187-202(1987).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88315049; PubMed=3045120;
 RA Gorman J.J., Nestorowicz A., Mitchell S.J., Corino G.L., Sellick P.W.;
 RT "Characterization of the sites of proteolytic activation of Newcastle disease virus membrane glycoprotein precursors.";
 RL J. Biol. Chem. 263:12522-12531(1988).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204897; PubMed=2705297;
 RA Sakaguchi T., Toyoda T., Goton B., Innocencio N.M., Kuma K., Miyata T., Nagai Y.;
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene.";
 RL Virology 169:260-272(1989).
 CC - FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING GLYCOPROTEINS.
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 CC - SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS N-TERMINAL HYDROPHOBIC SEQUENCE.
 CC - SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-NEURAMINIDASE FAMILY.
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FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 184 184 H -> HY (IN REF. 3).
FT CONFLICT 197 197 D -> H (IN REF. 1).
FT CONFLICT 259 259 E -> Q (IN REF. 1).
SQ SEQUENCE 570 AA; 62284 MW; 96EFJPFED67179D7 CRC64;

Query Match 91.3%; Score 2738.5; DB 1; Length 570;
Best Local Similarity 91.2%; Pred. No. 5.6e-209;
Matches 521; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

QY 1 MDRASQVLENDEREAKNTWRLIFRIALLTVTLATSVASLYSMGASTPSDLVGIP 60
DB 1 MNRVQVLENDEREAKNTWRLVFRILALLTVTLATSAALVSMGASTPSDLV 60
QY 61 TRISRAEKTSLAGSNQDVVDRIYKQVLESPLALNTETTMATISLSTQINGANN 120
DB 61 TRISRAEKTSLAGSNQDVVDRIYKQVLESPLALNTETTMATISLSTQINGANN 120
QY 121 SGNGAPIHDDPFTIGIGKELIVDNASDVTSFYPSPAFQEHNFIPATTTGGCTRI 180
DB 121 SGNGAPIHDDPFTIGIGKELIVDNASDVTSFYPSPAFQEHNFIPATTTGGCTRI 180
QY 181 SATHYCYTNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLSDDTQNRKSCSV 240
DB 181 SATH-CYTNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLSDDTQNRKSCSV 239
QY 241 SATPLGCDMLCSKVTEEBEDYNSAVPTLMAHRLGFDQYHEKDLDTTLFEDWV 300
DB 240 SATPLGCDMLCSKVTEEBEDYNSAVPTLMAHRLGFDQYHEKDLDTTLFEDWV 299
QY 301 GVGGSFIDGRWVFSYVGGKLPNSPDTVOEGKYVIYKRNDCPCPDQYQIRMASS 360
DB 300 GVGGSFIDGRWVFSYVGGKLPNSPDTVOEGKYVIYKRNDCPCPDQYQIRMASS 359
QY 361 PGRFGKRIQOAILSLKSVTSLGDEPVLTPPNTVTLMAGRILTVGTSHPLYOR 420
DB 360 PGRFGKRIQOAILSLKSVTSLGDEPVLTPPNTVTLMAGRILTVGTSHPLYOR 419
QY 421 FSPALLYPMVTNSKNTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDP 480
DB 420 FSPALLYPMVTNSKNTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDP 479
QY 481 NHTLRGVFGTMDSEORLNLVSAVDPNISRRIIRVSSSRITKAAVTTSTCFV 540
DB 480 NHTLRGVFGTMDSEORLNLVSAVDPNISRRIIRVSSSRITKAAVTTSTCFV 539
QY 541 YCLSIASISNTLFGEPRIVPLVEILLKNDGV 571
DB 540 YCLSIASISNTLFGEPRIVPLVEILLKNDGV 570

RESULT 12
HEMA NDVC STANDARD; PRT; 571 AA.
AC P35740;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN HN.
OS Newcastle disease virus (strain Ch1/85) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.
OX NCBI Taxid=11179;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=89204897; Pubmed=2705297;
RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. I. Multiple lineages defined by
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RT sequence variability of the hemagglutinin-neuraminidase gene.";
RL Virology 169:260-272(1989).
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CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC THE MATRE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC GLYCOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC N-TERMINAL HYDROPHOBIC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC NEURAMINIDASE FAMILY.
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CC -----
DR EMBL; M24716; AAA46666.1; -.
DR PIR; C36829; C36829.
DR InterPro; IPR000665; Hem-neuramidae.
DR Pfam; PF00423; HN; 1.
KW Hydroxylase, Hemagglutinin, Envelope protein; Glycoprotein;
KW Transmembrane.
FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 27 48 POTENTIAL.
FT DOMAIN 49 571 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 571 AA; 62901 MW; 3110CD668D71EF76 CRC64;

Query Match 90.4%; Score 2711; DB 1; Length 571;
Best Local Similarity 88.8%; Pred. No. 8.4e-207;
Matches 507; Conservative 32; Mismatches 32; Indels 0; Gaps 0;

QY 1 MDRASQVLENDEREAKNTWRLIFRIALLTVTLATSVASLYSMGASTPSDLVGIP 60
DB 1 MNRVQVLENDEREAKNTWRLVFRILALLTVTLATSAALVSMGASTPSDLV 60
QY 61 TRISRAEKTSLAGSNQDVVDRIYKQVLESPLALNTETTMATISLSTQINGANN 120
DB 61 TRISRAEKTSLAGSNQDVVDRIYKQVLESPLALNTETTMATISLSTQINGANN 120
QY 121 SGNGAPIHDDPFTIGIGKELIVDNASDVTSFYPSPAFQEHNFIPATTTGGCTRI 180
DB 121 SGNGAPIHDDPFTIGIGKELIVDNASDVTSFYPSPAFQEHNFIPATTTGGCTRI 180
QY 181 SATHYCYTNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLSDDTQNRKSCSV 240
DB 181 STTHYCYTNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLSDDTQNRKSCSV 240
QY 241 SATPLGCDMLCSKVTEEBEDYNSAVPTLMAHRLGFDQYHEKDLDTTLFEDWV 300
DB 241 SATPLGCDMLCSKVTEEBEDYNSAVPTLMAHRLGFDQYHEKDLDTTLFEDWV 300
QY 301 GVGGSFIDGRWVFSYVGGKLPNSPDTVOEGKYVIYKRNDCPCPDQYQIRMASS 360
DB 301 GVGGSFIDGRWVFSYVGGKLPNSPDTVOEGKYVIYKRNDCPCPDQYQIRMASS 360
QY 361 PGRFGKRIQOAILSLKSVTSLGDEPVLTPPNTVTLMAGRILTVGTSHPLYOR 420
DB 361 PGRFGKRIQOAILSLKSVTSLGDEPVLTPPNTVTLMAGRILTVGTSHPLYOR 420
QY 421 FSPALLYPMVTNSKNTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDP 480
```



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CC synthetic substrates.
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC N-TERMINAL HYDROPHOBIC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC NEURAMINIDASE FAMILY.
CC -----
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CC -----
DR EMBL; M62733; AAA47451.1; -
DR EMBL; X64275; CAA45568.1; -
DR PIR; A36419; HNNZ41.
DR InterPro; IPR000665; Hem-neuramidae.
DR Pfam; PF00423; HN; 1.
KW Hydroxylase; Hemagglutinin; Envelope protein; Glycoprotein;
KW Transmembrane.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 40
FT DOMAIN 41 568 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 44 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 568 AA; 61733 MW; 7C09738B2715F548 CRC64;

Query Match 28.0%; Score 838; DB 1; Length 568;
Best Local Similarity 35.0%; Pred. No. 1.5e-58;
Matches 203; Conservative 103; Mismatches 220; Indels 54; Gaps 11;

18 KNTWRLIFRIAILLVTLATSVASL---VYSGASTPSDLVIGIPTRISRAEKITSL 74
10 KRFFRAVFRILITLITLIALSMALYEVTHNSNGSESNQVDFDITLNA---ITGNI 66
75 GSNQDVDRIRYQVALESPLALNTETIMNATSLSYQNGAANSNGWAPHPDPEFG 134
67 KSMIALNLQILYNAAALPKIDSTESVLLAAKIDLFNSPASQNCSSGGLNDLALYN 126
135 GIGELILVDASDVTSFYPSAFQEHNL---FIPAPTTGSGCTRIPSPMATGYCTHNY 191
127 GINQYILSNFAGTIGLPL-----LNIPIFSATAPGCTRIPIPSLTIKTMCTSHNY 181
192 ILSGCRDHSHTOYALGVLRTATGRIFESTLRSISLDDTONRKCSCVSATPLGCDMLC 251
182 ILAGCADSKASNOYLMGIVGSSADPFPRTRMTTLVLSGINRKSQSVIAIFGGCALYC 241
252 SKYTEPEEDYINAVPTLMHGRIGFDGQYH-----EKIDVITTLFEDWANTPGVGGG 306
242 YVATKTEQEDYAAATPSEL---RLTF---YYNETLVERLTITIPVGTGNMATLNPAGSGV 296
307 FIDGRVWFVYGGGLKPSPDVQEGKYVLYKRINDCPDEODQUMASSYKPGFGG 366
297 YHGIYLAFPYGGILQNSAAMNSQFGSYFLPQNPAYOCSSAEOQITAGSYVWVMSG 356
367 KRIQOALISIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHPLYQSGSSYFSPALL 426
357 RLQSAVLVCPILSDQQLDQCRVVLFNNSSETMGEGRLYITIGDLYYYQSSSMWTASLL 416
427 Y-----PMYSNKTATILHSPTTNAFTPGSIFPCQASARCNCSVCTGYTDPY 475
417 YKINTDFSGQLPLIEAQWPTYLVP-----RPGAQPCASGFCPANCITGYADVMP 469
476 LI-----FYRNHTLRGVFGTMLDSEQARLNPAAVDSRSLRITVSSSSTKAA 526
470 KNNPFPAGSGGVNPNVJFGAF---LWADYARVAVPTFYMASATQYKNTTGFPSNQGA 526
527 TTSTCFKVVNTKNTYCLSLAIESNTLFGEPRIIVLLEIL 566
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DB 527 TTSTCFQNTGSKKIYCLFIEMGSSIMGEFOIVPFEIREVI 566

RESULT 15
ID HEMA_MUMPM STANDARD; PRT; 582 AA.
AC P11235;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN HN.
OS Mumps virus (strain Miyahara vaccine).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxId:11171;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89345175; PubMed=2762157;
RA Takeuchi K., Tanabayashi K., Hishiyama M., Yamada A., Sugitara A.;
RT "Cloning and sequencing of the haemagglutinin-neuraminidase gene of
RT mumps virus (Miyahara strain).";
RL Nucleic Acids Res. 17:5840-5840(1989).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC GLYCOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic acid and
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC N-TERMINAL HYDROPHOBIC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC NEURAMINIDASE FAMILY.
CC -----
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CC -----
DR EMBL; X15284; CAA33358.1; -
DR PIR; A34054; HNNZM.
DR InterPro; IPR000665; Hem-neuramidae.
DR Pfam; PF00423; HN; 1.
KW Hydroxylase; Hemagglutinin; Envelope protein; Glycoprotein;
KW Transmembrane.
FT DOMAIN 1 34 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 35 53 MEMBRANE ANCHOR (POTENTIAL).
FT DOMAIN 54 582 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 127 582 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 582 AA; 64044 MW; 9902600339625499 CRC64;

Query Match 26.1%; Score 781; DB 1; Length 582;
Best Local Similarity 33.8%; Pred. No. 5e-54;
Matches 194; Conservative 103; Mismatches 231; Indels 46; Gaps 15;

18 KNTWRLIFRIAILLVTLATSVASL---VYSGASTPSDLVIGIPTRISRAEKITSL 71
26 KTFRCFRLIFLVAVAVLLIVYTLGLVEMINDQGS--NQSLSDIKRESATMIA 83
72 SALGSDVDRIRYQVALESPLALNTETIMNATSL---SYQNGAANSNGWAP-1 127
```

Db 84 SAVG---VMOVHGVTVSLPLQIEGNQNOJLSTLATICGKXQVNSCSTN---IPLV 135
QY 128 HDPFIIIGIGIELIYDNAS-DVTSFYPAPFOEHLN--FIPAPTTGSGCTRIIPSPFMSAT 183
Db 136 NDLRFINGINKFIIEDYTHDFISGHP-----LMPSFIFPATSPNGCTRIIPSPFISLGT 189
QY 184 HCYTHNVILSGCRDHSHQYLAIVLRTATGRIFPSTLRISLDDTONRKSCSVSAT 243
Db 190 HMCYTHNVINANCMDHTSSNOYISMGILVQTAGYPMFKTLKIQYLSGLNRKSCSIATV 249
QY 244 PLGCDMLCSKYTEHEEDYNSAVPTLMAHGRIGPDQYHEKODVYTLFEDMVANYPGVG 303
Db 250 PDGCAMCYVSTOLETDDYAGSSPPTQKLTLLFYNDIVTERTISPTGLGNWATLVPGVG 309
QY 304 GGSFIDGRVWFSGGLKPNPSDVTQEGK--YVIYKRYNDTCPEODYQIRMAKSSYKP 361
Db 310 SGTYFENKLIIPAYGVLPNS-SLGVSAREPFRPNPYNPCSGEPQDLDQR-ALRSTYF 367
QY 362 GRFGGKRIQOAILSIKXSTSLGEDPVLTPPNTVTLMAEGRIILVTGSHFLYQSGSSYF 421
Db 368 SYFSNRVQSAFLVCAMNQIIVTNCELVPSNNOJLMGABGRVLLINNRLIYQGSTSW 427
QY 422 SPALLYPM---TVSNKTATLHSPYTENAFTRPQSIPOQASARCPNSCVTGVYTDYPLI 477
Db 428 PYELLYEISFTFTNSGQSSVMSWPIYSFTRPGSGNCGENVCPTACVSGVYLDPMPLT 487
QY 478 FYRHHTLRGV-----FCTMLDSEQARLNPASAVPDSRSTRITRVSSSTKAAYTSTC 531
Db 488 PYSHOS--GINRNFYFTGALLNSSTTRVNPFLYVSALNNKVLAPYGNQGLFASYTTTC 545
QY 532 FKVVYTNKTYCLISIAISNTLFGEEFRIVPLVEI 565
Db 546 FQDTGDASVYCVYIMELASNVGERQILPVLTRL 579

Search completed: January 2, 2004, 16:18:50
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:52 ; Search time 62 Seconds
(without alignments)
2401.554 Million cell updates/sec

Title: US-09-915-515A-1

Perfect score: 2998
Sequence: 1 MDRVSVQVALENDEREAKNT.....IVPLVETLKNQDVGREARSG 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_protist:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_unclassified:*
14: sp_virus:*
15: sp_bacterioph:*
16: sp_bacterioph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2998	100.0	577	12	Q9Q2W5 newcastie d
2	2926	97.6	577	12	Q9W8Z8 newcastie d
3	2920	97.4	577	12	Q83846 newcastie d
4	2920	97.4	577	12	Q90340 newcastie d
5	2917	97.3	577	12	Q91U00 newcastie d
6	2915	97.2	577	12	Q91AH7 newcastie d
7	2915	97.2	577	12	Q8B9S0 newcastie d
8	2913	97.2	577	12	Q83842 newcastie d
9	2902	96.8	577	12	Q9W9J0 newcastie d
10	2897	96.6	577	12	Q8BA53 newcastie d
11	2887	96.3	577	12	Q83844 newcastie d
12	2887	96.3	577	12	Q83845 newcastie d
13	2886	96.3	577	12	Q9WCW3 newcastie d
14	2863	95.5	577	12	Q89712 newcastie d
15	2860	95.4	577	12	Q83843 newcastie d
16	2838	94.7	616	12	Q83852 newcastie d

17	2821.5	94.1	615	12	Q83758 newcastie d
18	2801	93.4	572	12	Q56978 newcastie d
19	2748	91.7	572	12	Q56979 newcastie d
20	2746	91.6	571	12	Q83851 newcastie d
21	2746	91.6	571	12	Q91HD4 newcastie d
22	2730	91.1	571	12	Q73489 newcastie d
23	2727	91.0	571	12	Q9YN79 newcastie d
24	2726	90.9	571	12	Q9W9B1 newcastie d
25	2720	90.7	571	12	Q93161 newcastie d
26	2719.5	90.7	581	12	Q83850 newcastie d
27	2712	90.5	571	12	Q9W9I9 newcastie d
28	2703	90.2	571	12	Q9PYA4 newcastie d
29	2702	90.1	571	12	Q73490 newcastie d
30	2690	89.7	571	12	Q914X2 newcastie d
31	2687	89.6	571	12	Q8VIR0 newcastie d
32	2685	89.6	571	12	Q8VIR0 newcastie d
33	2684	89.5	571	12	Q91249 newcastie d
34	2681	89.4	571	12	Q8VIR1 newcastie d
35	2680	89.4	571	12	Q8VIR2 newcastie d
36	2667	89.0	571	12	Q83848 newcastie d
37	2667	89.0	571	12	Q8VIR0 newcastie d
38	2663	88.8	571	12	Q8J5X7 newcastie d
39	2662	88.8	571	12	Q9QCN6 newcastie d
40	2661	88.8	571	12	Q9W129 newcastie d
41	2658	88.7	571	12	Q9W9C3 newcastie d
42	2654	88.5	571	12	Q73491 newcastie d
43	2648	88.3	571	12	Q9YN78 newcastie d
44	1262	42.1	254	12	Q9E1T1 newcastie d
45	978	32.6	228	12	Q8BBT7 newcastie d

ALIGNMENTS

RESULT 1									
ID	Q9Q2W5	PRELIMINARY;	PRT;	577	AA.				
AC	Q9Q2W5;								
DT	01-MAY-2000 (TREMBLrel. 13, Created)								
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)								
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)								
DE	Hemagglutinin-neuraminidase glycoprotein.								
OS	Newcastle disease virus.								
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;								
OC	Paramyxoviridae; Paramyxovirinae; Rubulavirus.								
OX	NCBI_TaxID=11176;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Kansas;								
RX	MEDLINE=20238045; PubMed=10772993;								
RA	Takimoto T., Taylor G.L., Crennell S.J., Scroggs R.A., Portner A.;								
RT	"Crystallization of Newcastle disease virus hemagglutinin-								
RT	neuraminidase glycoprotein."								
RL	Virology 270:208-214 (2000).								
DR	EMBL; AF212323; AAF19984.1; -								
DR	InterPro: IPR000665; Hem-neuramidase.								
DR	Pfam: PF00423; HN; 1.								
DR	SEQUENCE 577 AA; 63111 MW; 6A1F03C8DD3F7753 CRC64;								
SQL	SEQUENCE 577 AA; 63111 MW; 6A1F03C8DD3F7753 CRC64;								
Query Match 100.0%; Score 2998; DB 12; Length 577;									
Best Local Similarity 100.0%; Pred. No. 1.9e-237;									
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0									
QY	1	MDRVSVQVALENDEREAKNTWRLIFRAILLLITVTTLATSVASLVYSGASTPSDVGIP	60						
DB	1	MDRVSVQVALENDEREAKNTWRLIFRAILLLITVTTLATSVASLVYSGASTPSDVGIP	60						
QY	61	TRISAREKITSALGSDVDVRIYKQVALESPLALNTETTINWATTSVQINGANN	120						
DB	61	TRISAREKITSALGSDVDVRIYKQVALESPLALNTETTINWATTSVQINGANN	120						
QY	121	SGWGAIPHDPFGIGIGELIVDNASDVTSFYPAPQEHILFIPAPTTGSGCTRIIPSPDM	180						

DB 121 SGWGAIPHDDPFIIGIGKELIVDNASDVTSFYPSPAFOEHLNFIAPPTGSGCTRIIPSPDM 180
QY 181 SATHYCYTHNVILSGCRDHSYQYLAAGVLTATTAATGRIFFSTLRISLDDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHSYQYLAAGVLTATTAATGRIFFSTLRISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFDQYHEKLDVTLTFEDWVANYP 300
DB 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFDQYHEKLDVTLTFEDWVANYP 300
QY 301 GVGGGSEFIDGRVWFSYGGGLKPNSPDPTVOEGKVIYKRYNDTCPEBODYQIRMAKSSYK 360
DB 301 GVGGGSEFIDGRVWFSYGGGLKPNSPDPTVOEGKVIYKRYNDTCPEBODYQIRMAKSSYK 360
QY 361 PGRFGGRIQOAILSTIKVSTSLGDEPVLTPPNTVTLMGABGRILTVGSHFLYORGSSY 420
DB 361 PGRFGGRIQOAILSTIKVSTSLGDEPVLTPPNTVTLMGABGRILTVGSHFLYORGSSY 420
QY 421 FSPALLYPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCNSCVTVGYTDPYPLIFR 480
DB 421 FSPALLYPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCNSCVTVGYTDPYPLIFR 480
QY 481 NHTLRGVFTMLDSEQARLNPASAVFDSTSRIRTRVSSSTKAAVTTSTCFKVVYKTKNT 540
DB 481 NHTLRGVFTMLDSEQARLNPASAVFDSTSRIRTRVSSSTKAAVTTSTCFKVVYKTKNT 540
QY 541 YCLSTAEISNTLFGERRIVPLVEILKNDGVREARSG 577
DB 541 YCLSTAEISNTLFGERRIVPLVEILKNDGVREARSG 577

RESULT 2

Q9W8Z8 PRELIMINARY; PRT; 577 AA.

AC Q9W8Z8; 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hemagglutinin-neuraminidase.
GN HN.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
OX NCBI_TaxId=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VACCINE-RUS LA SOTA TYPE);
RA Gribanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,
RT "Phylogenetic analysis of Newcastle disease virus of Russia."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VACCINE-RUS;
RA Gribanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,
RT "Phylogenetic analysis of Newcastle disease virus of Russia."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=VACCINE-RUS;
RA Gribanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,
RT "Phylogenetic analysis of Newcastle disease virus of Russia."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EMBL: Y19020; CAB50911.1; -
EMBL: Y18726; CAAT7272.1; -
EMBL: AJ243386; CAB46067.1; -
DR InterPro: IPR000665; Hem-neuramndse.
DR Pfam: PF00423; HN; 1.
SQ SEQUENCE 577 AA; 63153 MW; D4FCBA45ECDB089 CRC64;

Query Match 97.6%; Score 2926; DB 12; Length 577;

Best Local Similarity 97.2%; Pred. No. 1.6e-231;
Matches 561; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
QY 1 MRAVSQVLENDERAKNTWLRIRIATLLTWTTLASVASLYSMGASTPSDVGIP 60
DB 1 MRAVSQVLENDERAKNTWLRIRIATLLTWTTLASVASLYSMGASTPSDVGIP 60
QY 61 TRISRAEEKITSLGSDQVNDRIYKQVALESPALLNTEETIMATLSLQINGAANN 120
DB 61 TRISRAEEKITSLGSDQVNDRIYKQVALESPALLNTEETIMATLSLQINGAANN 120
QY 121 SGWGAIPHDDPFIIGIGKELIVDNASDVTSFYPSPAFOEHLNFIAPPTGSGCTRIIPSPDM 180
DB 121 SGWGAIPHDDPFIIGIGKELIVDNASDVTSFYPSPAFOEHLNFIAPPTGSGCTRIIPSPDM 180
QY 181 SATHYCYTHNVILSGCRDHSYQYLAAGVLTATTAATGRIFFSTLRISLDDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHSYQYLAAGVLTATTAATGRIFFSTLRISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFDQYHEKLDVTLTFEDWVANYP 300
DB 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFDQYHEKLDVTLTFEDWVANYP 300
QY 301 GVGGGSEFIDGRVWFSYGGGLKPNSPDPTVOEGKVIYKRYNDTCPEBODYQIRMAKSSYK 360
DB 301 GVGGGSEFIDGRVWFSYGGGLKPNSPDPTVOEGKVIYKRYNDTCPEBODYQIRMAKSSYK 360
QY 361 PGRFGGRIQOAILSTIKVSTSLGDEPVLTPPNTVTLMGABGRILTVGSHFLYORGSSY 420
DB 361 PGRFGGRIQOAILSTIKVSTSLGDEPVLTPPNTVTLMGABGRILTVGSHFLYORGSSY 420
QY 421 FSPALLYPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCNSCVTVGYTDPYPLIFR 480
DB 421 FSPALLYPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCNSCVTVGYTDPYPLIFR 480
QY 481 NHTLRGVFTMLDSEQARLNPASAVFDSTSRIRTRVSSSTKAAVTTSTCFKVVYKTKNT 540
DB 481 NHTLRGVFTMLDSEQARLNPASAVFDSTSRIRTRVSSSTKAAVTTSTCFKVVYKTKNT 540
QY 541 YCLSTAEISNTLFGERRIVPLVEILKNDGVREARSG 577
DB 541 YCLSTAEISNTLFGERRIVPLVEILKNDGVREARSG 577

RESULT 3

Q83846 PRELIMINARY; PRT; 577 AA.

AC Q83846; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hemagglutinin-neuraminidase.
GN HN.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
OX NCBI_TaxId=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B1 (SBPR);
RA Seal B.S., King D.J., Bennett J.D.;
RT "Characterization of Newcastle disease virus vaccines by biological
RT properties and sequence analysis of the hemagglutinin-neuraminidase
RT protein gene."
RL Vaccine 14:761-766 (1996).
EMBL: U37193; AAC55047.1; -
DR InterPro: IPR000665; Hem-neuramndse.
DR Pfam: PF00423; HN; 1.
SQ SEQUENCE 577 AA; 63215 MW; 886FA85D3A885404 CRC64;

Query Match 97.4%; Score 2920; DB 12; Length 577;
Best Local Similarity 96.9%; Pred. No. 4.9e-231;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;


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QY 1 MDRASQVLAENDEREAKNTWRLIFRIAILLTVTTLATSVASLVYSGASTPSDLVIGIP 60
Db 1 MDRASQVLAENDEREAKNTWRLIFRIAILLTVTTLATSVASLVYSGASTPSDLVIGIP 60
QY 61 TRIRAEKITSALGSNDVDRIYKQVLAESPALANTETTINMAITSLSYOINGAANN 120
Db 61 TRIRAEKITSALGSNDVDRIYKQVLAESPALANTETTINMAITSLSYOINGAANN 120
QY 121 SGWGAPIHDPDPIGIGIKELIVDNASDVTSFYPSPAFQEHNFIPAPTTGSGCTRIPSFDM 180
Db 121 SGWGAPIHDPDPIGIGIKELIVDNASDVTSFYPSPAFQEHNFIPAPTTGSGCTRIPSFDM 180
QY 181 SATHYCTHNVILSGCRDHSYQYALGVLRRTATGRIFPSTLRSLSDTQNRKSCSV 240
Db 181 SATHYCTHNVILSGCRDHSYQYALGVLRRTATGRIFPSTLRSLSDTQNRKSCSV 240
QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFDGQYHEKOLDVTTLFEPMVANYP 300
Db 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFDGQYHEKOLDVTTLFEPMVANYP 300
QY 301 GVGGGSFIDGRWVSVYGLKPNPSDPTVQEGKVIYKRYNDTCPEDDQYQIRMAKSSYK 360
Db 301 GVGGGSFIDGRWVSVYGLKPNPSDPTVQEGKVIYKRYNDTCPEDDQYQIRMAKSSYK 360
QY 361 PGRGGRKIQOALISIKVSTSLGEDPVLTPPNTVTLMAGRILITVGTSHFLYQORSSY 420
Db 361 PGRGGRKIQOALISIKVSTSLGEDPVLTPPNTVTLMAGRILITVGTSHFLYQORSSY 420
QY 421 FSPALLPMTVSNKTATLHSPYTFNATFRPGSIPCOASARCPNSCVGVTDPPPLFYR 480
Db 421 FSPALLPMTVSNKTATLHSPYTFNATFRPGSIPCOASARCPNSCVGVTDPPPLFYR 480
QY 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRITRVSSSTKAAYTSTCFKVKTKNTK 540
Db 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRITRVSSSTKAAYTSTCFKVKTKNTK 540
QY 541 YCLSIASISNTLFGFRIPLVLEILKNDGVEARSG 577
Db 541 YCLSIASISNTLFGFRIPLVLEILKNDGVEARSG 577

RESULT 4
090340 PRELIMINARY; PRT; 577 AA.
AC 090340;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hemagglutinin-neuraminidase.
GN HN.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=LASOTA;
RA de Leeuw O.S.; Peeters B.P.H.;
RT "Complete nucleotide sequence of Newcastle disease virus: evidence for
RT the existence of a new genus within the subfamily Paramyxovirinae.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=B1;
RA Roemer-Oberdorfer A.; Buchholz U.J.; Mundt E.; Mettenleiter T.C.;
RT "Generation of recombinant lentogenic Newcastle Virus from
RT CDNA.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Roemer-Oberdorfer A.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF077761; AAC28376.1; -

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DR EMBL; Y18898; CAB51326.1; -
DR InterPro; IPR000665; Hem-neuramde.
DR Pfam; PF00423; HN; 1.
SQ SEQUENCE 577 AA; 63213 MW; 66D63FALB3041EB4 CRC64;

Query Match 97.4%; Score 2920; DB 12; Length 577;
Best local similarity 97.1%; Pred. No. 4.9e-231;
Matches 560; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDRASQVLAENDEREAKNTWRLIFRIAILLTVTTLATSVASLVYSGASTPSDLVIGIP 60
Db 1 MDRASQVLAENDEREAKNTWRLIFRIAILLTVTTLATSVASLVYSGASTPSDLVIGIP 60
QY 61 TRIRAEKITSALGSNDVDRIYKQVLAESPALANTETTINMAITSLSYOINGAANN 120
Db 61 TRIRAEKITSALGSNDVDRIYKQVLAESPALANTETTINMAITSLSYOINGAANN 120
QY 121 SGWGAPIHDPDPIGIGIKELIVDNASDVTSFYPSPAFQEHNFIPAPTTGSGCTRIPSFDM 180
Db 121 SGWGAPIHDPDPIGIGIKELIVDNASDVTSFYPSPAFQEHNFIPAPTTGSGCTRIPSFDM 180
QY 181 SATHYCTHNVILSGCRDHSYQYALGVLRRTATGRIFPSTLRSLSDTQNRKSCSV 240
Db 181 SATHYCTHNVILSGCRDHSYQYALGVLRRTATGRIFPSTLRSLSDTQNRKSCSV 240
QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFDGQYHEKOLDVTTLFEPMVANYP 300
Db 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRIGFDGQYHEKOLDVTTLFEPMVANYP 300
QY 301 GVGGGSFIDGRWVSVYGLKPNPSDPTVQEGKVIYKRYNDTCPEDDQYQIRMAKSSYK 360
Db 301 GVGGGSFIDGRWVSVYGLKPNPSDPTVQEGKVIYKRYNDTCPEDDQYQIRMAKSSYK 360
QY 361 PGRGGRKIQOALISIKVSTSLGEDPVLTPPNTVTLMAGRILITVGTSHFLYQORSSY 420
Db 361 PGRGGRKIQOALISIKVSTSLGEDPVLTPPNTVTLMAGRILITVGTSHFLYQORSSY 420
QY 421 FSPALLPMTVSNKTATLHSPYTFNATFRPGSIPCOASARCPNSCVGVTDPPPLFYR 480
Db 421 FSPALLPMTVSNKTATLHSPYTFNATFRPGSIPCOASARCPNSCVGVTDPPPLFYR 480
QY 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRITRVSSSTKAAYTSTCFKVKTKNTK 540
Db 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRITRVSSSTKAAYTSTCFKVKTKNTK 540
QY 541 YCLSIASISNTLFGFRIPLVLEILKNDGVEARSG 577
Db 541 YCLSIASISNTLFGFRIPLVLEILKNDGVEARSG 577

RESULT 5
091U10 PRELIMINARY; PRT; 577 AA.
AC 091U10;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hemagglutinin-neuraminidase.
GN HN.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=B1;
RA Sellers H.S.; Seal B.S.;
RT "Complete sequence for the B1 strain of Newcastle disease virus.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309418; AAC36979.1; -
DR InterPro; IPR000665; Hem-neuramde.
DR Pfam; PF00423; HN; 1.
SQ SEQUENCE 577 AA; 63227 MW; 23D6748352C8C17 CRC64;

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Query Match 97.3%; Score 2917; DB 12; Length 577;
 Best Local Similarity 96.9%; Pred. No. 8.7e-231;
 Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

1 MDRASQVALENDEREAKNTWRLIFRIAILLTVVTALTSVASLYSMGASTPSDLVGP 60
 1 MDRASQVALENDEREAKNTWRLIFRIAILLTVVTALTSVASLYSMGASTPSDLVGP 60
 61 TRISRAEEKITSLGSDNOVDRIYKQVALESPALLNTEITMNAITSLSYQINGAANN 120
 61 TRISRAEEKITSLGSDNOVDRIYKQVALESPALLNTEITMNAITSLSYQINGAANN 120
 121 SGCGAPIHDPDITGIGKELIYDNASDVTSFYPSPAFQEHNFIPAPPTGSGCTRIIPSPDM 180
 121 SGCGAPIHDPDITGIGKELIYDNASDVTSFYPSPAFQEHNFIPAPPTGSGCTRIIPSPDM 180
 181 SATHYCYTHNVILSGCRDHS HQYLALGVLTARTAGRIFFSTLRSISLDDTONRKSCSV 240
 181 SATHYCYTHNVILSGCRDHS HQYLALGVLTARTAGRIFFSTLRSISLDDTONRKSCSV 240
 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGLGPDQYHEKDLDTTLFEDWVANY 300
 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGLGPDQYHEKDLDTTLFEDWVANY 300
 301 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
 301 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
 361 GVRFGKRIQOAILSIKYSTSLGEPVLTPPNTVTLMAGRIILTVGSHFLYQSGSSY 420
 361 GVRFGKRIQOAILSIKYSTSLGEPVLTPPNTVTLMAGRIILTVGSHFLYQSGSSY 420
 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCNSCVGYVTDYPLIFXR 480
 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCNSCVGYVTDYPLIFXR 480
 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSSKAAVYTSCTCKVYKTKNT 540
 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSSKAAVYTSCTCKVYKTKNT 540
 541 YCLISAEISNTLFGFRIPLVLEILKNDGVREARSG 577
 541 YCLISAEISNTLFGFRIPLVLEILKNDGVREARSG 577

RESULT 6

Q91AH7 PRELIMINARY; PRT; 577 AA.
 AC Q91AH7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hemagglutinin-neuraminidase.
 GN HN.
 OS Newcastle disease virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
 OC NCBI_TaxID=11176;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B1;
 RX MEDLINE=21548317; PubMed=11689668;
 RA Nakaya T., Cros J., Park M.S., Nakaya Y., Zheng H., Sagstera A.,
 Villar E., Garcia-Sastre A., Palese P.;
 RT "Recombinant newcastle disease virus as a vaccine vector.";
 RT J. Virol. 75:11868-11873(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B1;
 RA Nakaya T., Garcia-Sastre A., Palese P.;
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF375823; AAK55551.1; -.

DR InterPro; IPR000665; Hem-neuramidae.
 DR Pfam; PF00423; HN.1.
 SQ SEQUENCE 577 AA; 63216 MW; D5A26F305A885969 CRC64;

Query Match 97.2%; Score 2915; DB 12; Length 577;
 Best Local Similarity 96.7%; Pred. No. 1.3e-230;
 Matches 558; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

1 MDRASQVALENDEREAKNTWRLIFRIAILLTVVTALTSVASLYSMGASTPSDLVGP 60
 1 MDRASQVALENDEREAKNTWRLIFRIAILLTVVTALTSVASLYSMGASTPSDLVGP 60
 61 TRISRAEEKITSLGSDNOVDRIYKQVALESPALLNTEITMNAITSLSYQINGAANN 120
 61 TRISRAEEKITSLGSDNOVDRIYKQVALESPALLNTEITMNAITSLSYQINGAANN 120
 121 SGCGAPIHDPDITGIGKELIYDNASDVTSFYPSPAFQEHNFIPAPPTGSGCTRIIPSPDM 180
 121 SGCGAPIHDPDITGIGKELIYDNASDVTSFYPSPAFQEHNFIPAPPTGSGCTRIIPSPDM 180
 181 SATHYCYTHNVILSGCRDHS HQYLALGVLTARTAGRIFFSTLRSISLDDTONRKSCSV 240
 181 SATHYCYTHNVILSGCRDHS HQYLALGVLTARTAGRIFFSTLRSISLDDTONRKSCSV 240
 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGLGPDQYHEKDLDTTLFEDWVANY 300
 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGLGPDQYHEKDLDTTLFEDWVANY 300
 301 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
 301 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
 361 GVRFGKRIQOAILSIKYSTSLGEPVLTPPNTVTLMAGRIILTVGSHFLYQSGSSY 420
 361 GVRFGKRIQOAILSIKYSTSLGEPVLTPPNTVTLMAGRIILTVGSHFLYQSGSSY 420
 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCNSCVGYVTDYPLIFXR 480
 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCNSCVGYVTDYPLIFXR 480
 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSSKAAVYTSCTCKVYKTKNT 540
 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSSKAAVYTSCTCKVYKTKNT 540
 541 YCLISAEISNTLFGFRIPLVLEILKNDGVREARSG 577
 541 YCLISAEISNTLFGFRIPLVLEILKNDGVREARSG 577

RESULT 7

Q8B9S0 PRELIMINARY; PRT; 577 AA.
 AC Q8B9S0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hemagglutinin-neuraminidase protein HN.
 OS Newcastle disease virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
 OC NCBI_TaxID=11176;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MET95;
 RA Murakawa Y., Sakaguchi M., Soejima K., Friguchi S., Takase K.,
 Sueyoshi M., Nagatomo H., Ito T., Otsuki K.;
 RT "Haemagglutinating activity of the lentogenic Newcastle disease virus
 strain MET95.";
 RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY143159; AAM18268.1; -.
 SQ SEQUENCE 577 AA; 63269 MW; 1B3EA99008B5AF42 CRC64;

Query Match 97.2%; Score 2915; DB 12; Length 577;

Best Local Similarity 96.5%, Pred. No. 1.3e-230;
Matches 557; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MDRASQVLENDEREAKNTWRLIFRIAILLTAVTATSVASLVYSGASTPSDLVGP 60
Db 1 MDRASQVLENDEREAKNTWRLIFRIAILLTAVTATSVASLVYSGASTPSDLVGP 60
QY 61 TRISRAEKKITSAIGSNODVVDRIYKQVLESPLALNTETTINMAITSLSYQINGAAN 120
Db 61 TRISRAEKKITSAIGSNODVVDRIYKQVLESPLALNTETTINMAITSLSYQINGAAN 120
QY 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSDM 180
Db 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSDM 180
QY 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSDM 180
Db 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSDM 180
QY 181 SATHYCTTHNVILSGCRDHSYQYLAGVLRATATGRIFPSTLRSLDPTORRKSQSV 240
Db 181 SATHYCTTHNVILSGCRDHSYQYLAGVLRATATGRIFPSTLRSLDPTORRKSQSV 240
QY 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFEDMVANYP 300
QY 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFEDMVANYP 300
QY 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
QY 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMGAGRLITVGTSHFLYQSGSY 420
Db 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMGAGRLITVGTSHFLYQSGSY 420
QY 421 FSPALLPMTVSNKTATLHSPYENAFTRPGSIFPCQASARCPNSCVTVYDPIPLFYR 480
Db 421 FSPALLPMTVSNKTATLHSPYENAFTRPGSIFPCQASARCPNSCVTVYDPIPLFYR 480
QY 421 FSPALLPMTVSNKTATLHSPYENAFTRPGSIFPCQASARCPNSCVTVYDPIPLFYR 480
Db 421 FSPALLPMTVSNKTATLHSPYENAFTRPGSIFPCQASARCPNSCVTVYDPIPLFYR 480
QY 481 NHTLRGVFGTMDSEQARLPASAVFDSTSRSTRITRVSSSTKAAYTSTCFKVKTKNT 540
Db 481 NHTLRGVFGTMDSEQARLPASAVFDSTSRSTRITRVSSSTKAAYTSTCFKVKTKNT 540
QY 541 YCLSIASISNTLFGFPRIVPLVEILKDDGVREARSG 577
Db 541 YCLSIASISNTLFGFPRIVPLVEILKDDGVREARSG 577
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RESULT 8

083842 PRELIMINARY; PRT; 577 AA.

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AC 083842;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hemagglutinin-neuraminidase.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae;
OC NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAH/85;
RA MEDLINE=96414821; PubMed=8817822;
RA Seal B.S., King D.J., Bennett J.D.;
RT "Characterization of Newcastle disease virus vaccines by biological
RT properties and sequence analysis of the hemagglutinin-neuraminidase
RT protein gene."
RL Vaccine 14:761-766 (1996).
DR EMBL; U37187; AAC55041.1;
DR InterPro; IPR000665; Hem-neuramds.
DR Pfam; PF00423; HN; 1.
SQ SEQUENCE 577 AA; 63213 MM; 59DEF068352C8C16 CRC64;
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Query Match 97.2%; Score 2913; DB 12; Length 577;
Best Local Similarity 96.7%; Pred. No. 1.9e-230;
Matches 558; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

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QY 1 MDRASQVLENDEREAKNTWRLIFRIAILLTAVTATSVASLVYSGASTPSDLVGP 60
Db 1 MDRASQVLENDEREAKNTWRLIFRIAILLTAVTATSVASLVYSGASTPSDLVGP 60
QY 61 TRISRAEKKITSAIGSNODVVDRIYKQVLESPLALNTETTINMAITSLSYQINGAAN 120
Db 61 TRISRAEKKITSAIGSNODVVDRIYKQVLESPLALNTETTINMAITSLSYQINGAAN 120
QY 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSDM 180
Db 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSDM 180
QY 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSDM 180
Db 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSDM 180
QY 181 SATHYCTTHNVILSGCRDHSYQYLAGVLRATATGRIFPSTLRSLDPTORRKSQSV 240
Db 181 SATHYCTTHNVILSGCRDHSYQYLAGVLRATATGRIFPSTLRSLDPTORRKSQSV 240
QY 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFEDMVANYP 300
QY 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGFGQYHEKDLVTTLFEDMVANYP 300
QY 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
QY 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMGAGRLITVGTSHFLYQSGSY 420
Db 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMGAGRLITVGTSHFLYQSGSY 420
QY 421 FSPALLPMTVSNKTATLHSPYENAFTRPGSIFPCQASARCPNSCVTVYDPIPLFYR 480
Db 421 FSPALLPMTVSNKTATLHSPYENAFTRPGSIFPCQASARCPNSCVTVYDPIPLFYR 480
QY 421 FSPALLPMTVSNKTATLHSPYENAFTRPGSIFPCQASARCPNSCVTVYDPIPLFYR 480
Db 421 FSPALLPMTVSNKTATLHSPYENAFTRPGSIFPCQASARCPNSCVTVYDPIPLFYR 480
QY 481 NHTLRGVFGTMDSEQARLPASAVFDSTSRSTRITRVSSSTKAAYTSTCFKVKTKNT 540
Db 481 NHTLRGVFGTMDSEQARLPASAVFDSTSRSTRITRVSSSTKAAYTSTCFKVKTKNT 540
QY 541 YCLSIASISNTLFGFPRIVPLVEILKDDGVREARSG 577
Db 541 YCLSIASISNTLFGFPRIVPLVEILKDDGVREARSG 577
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RESULT 9

09W9H0 PRELIMINARY; PRT; 577 AA.

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AC 09W9H0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hemagglutinin-neuraminidase.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae;
OC NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAH/85;
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,
RA Grisev A.A., Balyshay V.M., Zhesterev V.I., Vishnjakov I.F.;
RT "Phylogenetic analysis of Newcastle disease virus of Russia."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SAH/85;
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,
RA Grisev A.A., Balyshay V.M., Zhesterev V.I., Vishnjakov I.F.;
RT "Phylogenetic analysis of Newcastle disease virus of Russia."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y19021; CAB50912.1;
DR EMBL; AJ243384; CAB46065.1;
DR InterPro; IPR000665; Hem-neuramds.
DR Pfam; PF00423; HN; 1.
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SQL SEQUENCE 577 AA; 63181 MW; E2C045E98F8EAAA CRC64;
Query Match 96.8%; Score 2902; DB 12; Length 577;
Best Local Similarity 96.4%; Pred. No. 1.5e-229;
Matches 556; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
QY 1 MORAVALLENDEREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGIP 60
DB 1 MORAVALLENDEREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGIP 60
QY 61 TRISRAEEKITSLAGSNODVVDRIYKQVLESPLALNTETTTMAITSLSYQINGAANN 120
DB 61 TRISRAEEKITSLAGSNODVVDRIYKQVLESPLALNTETTTMAITSLSYQINGAANN 120
QY 61 TRISRAEEKITSLAGSNODVVDRIYKQVLESPLALNTETTTMAITSLSYQINGAANN 120
DB 61 TRISRAEEKITSLAGSNODVVDRIYKQVLESPLALNTETTTMAITSLSYQINGAANN 120
QY 121 SCMGAPLHDPDFIGIGKELIVDNASDVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPFM 180
DB 121 SCMGAPLHDPDFIGIGKELIVDNASDVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPFM 180
QY 121 SCMGAPLHDPDFIGIGKELIVDNASDVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPFM 180
DB 121 SCMGAPLHDPDFIGIGKELIVDNASDVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPFM 180
QY 181 SATHYCYTNHVLISGCRDHS HQYLALGVLTATGRIIPFSTLRSISLDDTONRKSCSV 240
DB 181 SATHYCYTNHVLISGCRDHS HQYLALGVLTATGRIIPFSTLRSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKVETEEDYNASAVPTLMAHGRIGFDQYHEKLDVTTLPEDWYANP 300
DB 241 SATPLGCDMLCSKVETEEDYNASAVPTLMAHGRIGFDQYHEKLDVTTLPEDWYANP 300
QY 301 GVGGSFIDGRVWFVSYGGLKPNPSDPTVQEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
DB 301 GVGGSFIDGRVWFVSYGGLKPNPSDPTVQEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSLIKVSTSLGEBPVLTPPNTVTLMAEGRILLVGTSHFLYORGSSY 420
DB 361 PGRFGKRIQOAILSLIKVSTSLGEBPVLTPPNTVTLMAEGRILLVGTSHFLYORGSSY 420
QY 421 FSPALLPYMTVSNKATLHSPYTFNAPTRPGSIPCOASARCPNSCVTGYTDPYPLIFR 480
DB 421 FSPALLPYMTVSNKATLHSPYTFNAPTRPGSIPCOASARCPNSCVTGYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSTKAAVYTSICFKVYKTKNT 540
DB 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSTKAAVYTSICFKVYKTKNT 540
QY 541 YCLSTIAEISNTLFGERRIYPLVLEILKNDGVREARSG 577
DB 541 YCLSTIAEISNTLFGERRIYPLVLEILKNDGVREARSG 577
RESULT 10
Q8BA53 PRELIMINARY; PRT; 577 AA.
AC Q8BA53;
DB 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Hemagglutinin-neuraminidase.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=23/2000;
RA Zhou J.Y., Ye J.X., Chen Q.X., Wang J.Y., Chen J.G., Cheng L.Q.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY135171; AAN08047.1; -
SQ SEQUENCE 577 AA; 63236 MW; 5EBCA979387AB3A CRC64;
Query Match 96.6%; Score 2897; DB 12; Length 577;
Best Local Similarity 96.4%; Pred. No. 3.8e-229;
Matches 556; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
QY 1 MORAVALLENDEREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGIP 60
DB 1 MORAVALLENDEREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGIP 60

DB 1 MORAVALLENDEREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGIP 60
QY 61 TRISRAEEKITSLAGSNODVVDRIYKQVLESPLALNTETTTMAITSLSYQINGAANN 120
DB 61 TRISRAEEKITSLAGSNODVVDRIYKQVLESPLALNTETTTMAITSLSYQINGAANN 120
QY 121 SCMGAPLHDPDFIGIGKELIVDNASDVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPFM 180
DB 121 SCMGAPLHDPDFIGIGKELIVDNASDVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPFM 180
QY 121 SCMGAPLHDPDFIGIGKELIVDNASDVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPFM 180
DB 121 SCMGAPLHDPDFIGIGKELIVDNASDVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPFM 180
QY 181 SATHYCYTNHVLISGCRDHS HQYLALGVLTATGRIIPFSTLRSISLDDTONRKSCSV 240
DB 181 SATHYCYTNHVLISGCRDHS HQYLALGVLTATGRIIPFSTLRSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKVETEEDYNASAVPTLMAHGRIGFDQYHEKLDVTTLPEDWYANP 300
DB 241 SATPLGCDMLCSKVETEEDYNASAVPTLMAHGRIGFDQYHEKLDVTTLPEDWYANP 300
QY 301 GVGGSFIDGRVWFVSYGGLKPNPSDPTVQEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
DB 301 GVGGSFIDGRVWFVSYGGLKPNPSDPTVQEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSLIKVSTSLGEBPVLTPPNTVTLMAEGRILLVGTSHFLYORGSSY 420
DB 361 PGRFGKRIQOAILSLIKVSTSLGEBPVLTPPNTVTLMAEGRILLVGTSHFLYORGSSY 420
QY 421 FSPALLPYMTVSNKATLHSPYTFNAPTRPGSIPCOASARCPNSCVTGYTDPYPLIFR 480
DB 421 FSPALLPYMTVSNKATLHSPYTFNAPTRPGSIPCOASARCPNSCVTGYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSTKAAVYTSICFKVYKTKNT 540
DB 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSTKAAVYTSICFKVYKTKNT 540
QY 541 YCLSTIAEISNTLFGERRIYPLVLEILKNDGVREARSG 577
DB 541 YCLSTIAEISNTLFGERRIYPLVLEILKNDGVREARSG 577
RESULT 11
Q83844 PRELIMINARY; PRT; 577 AA.
AC Q83844;
DB 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Hemagglutinin-neuraminidase.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=vaccine 4;
RA MEDLINE=96414821; PubMed=8817822;
RA Seal B.S., King D.J., Bennett J.D.;
RT "Characterization of Newcastle disease virus vaccines by biological
RT properties and sequence analysis of the hemagglutinin-neuraminidase
RT protein gene."
RL Vaccine 14:761-766 (1996).
DR EMBL; U37190; AAC55044.1; -
DR InterPro; IPR000665; Hem-neuramdee.
DR Pfam; PR00423; HN.1
SQ SEQUENCE 577 AA; 63231 MW; ACC95422982CT878 CRC64;
Query Match 96.3%; Score 2887; DB 12; Length 577;
Best Local Similarity 95.7%; Pred. No. 2.5e-228;
Matches 552; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
QY 1 MORAVALLENDEREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGIP 60
DB 1 MORAVALLENDEREAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGIP 60

Qy	61	RRISAEEKITSLALCSNOVDRIKQVWALLESPIALNFMETIMNAITSLISVYOINGAANN	120
Db	61	TRISAEEKITSLALCSNOVDRIKQVWALLESPIALNFMETIMNAITSLISVYOINGAANN	120
Qy	121	SGMGAPIHDPDEIGIGIKELIVDNASDVTSFYPSAFOEHLNFIAPBTTGSGCTRIPSPDM	180
Db	121	SGMGAPIHDPDEIGIGIKELIVDDASDVTSFYPSAFOEHLNFIAPBTTGSGCTRIPSPDM	180
Qy	181	SATHCYTHNYLISGCRDHSHTOYALAGVLTATAGRIFFESTLBSISLDPONRSCSV	240
Db	181	SATHCYTHNYLISGCRDHSHTOYALISLVLRITSAGRVFPSTLRISINDDPONRSCSV	240
Qy	241	SATPLGCDMLCSKVETEBEEDYNASAVPTLMAHGRGLDFDQYHEKDDVTLTFEDWANYAP	300
Db	241	SATPLGCDMLCSKVETEBEEDYNASAVPTMAHGRGLDFDQYHEKDDVTLTFEDWANYAP	300
Qy	301	GVGGGSFLDGRWFSEVVGGLKPNSSBDTVQEGKYVYKRYNTPCPEBODYQIRMASSYK	360
Db	301	GVGGGSFLDGRWFSEVVGGLKPNSSBDTVQEGKYVYKRYNTPCPEBODYQIRMASSYK	360
Qy	361	PGRFEGKRIQOALISIKVSTSLGEDPVLTVPENTVTILMAEGRLILVGTSHFLYQRGSSY	420
Db	361	PGRFEGKRIQOALISIKVSTSLGEDPVLTVPENTVTILMAEGRLILVGTSHFLYQRGSSY	420
Qy	421	FSPALLYPMYVSNKTAATLHSPYTFNAFTFPGSIPCOASARCPNCSYGYTDBYPLIFR	480
Db	421	FSPALLYPMYVSNKTAATLHSPYTFNAFTFPGSIPCOASARCPNCSYGYTDBYPLIFR	480
Qy	481	NHTLRGVGTMLDSEQARLNPPASAFVSDSTRSRIRTVSSSSSTKAAATTSITCFKVVYTNKT	540
Db	481	NHTLRGVGTMLDGOARLNPPASAFVSDSTRSRIRTVSSSSSTKAAATTSITCFKVVYTNKT	540
Qy	541	YCLSLAELISNTLFGFRIYVPLLVLEILKNDGVREARSG	577
Db	541	YCLSLAELISNTLFGFRIYVPLLVLEILKNDGVREARSG	577

	RESULT	12			
ID	Q83845		PRELIMINARY;	PRT;	577 AA.
AC	Q83845;				
DT	01-NOV-1996	(TREMBLrel. 01,			
DT	01-NOV-1996	(TREMBLrel. 01,			
DT	01-JUN-2001	(TREMBLrel. 17,			
DE	Hemagglutinin-neuraminidase.				
OS	Viruslike disease virus.				
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;				
OC	Paramyxoviridae; Paramyxovirinae; Rubulavirus.				
OX	NCBI_TaxID=11176;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=vaccine 5;				
RX	MEDLINE=96414821; PubMed=8617822;				
RA	Seal B.S., King D.J., Bennett J.D.;				
RT	"Characterization of Newcastle disease virus vaccines by biological				
RT	properties and sequence analysis of the hemagglutinin-neuraminidase				
RT	protein gene.";				
RL	Vaccine 14:761-766(1996).				
DR	EMBL, U37191; AACS5045.1; -.				
DR	InterPro; IPR000665; Hem-neuramdbae.				
DR	Pfam; PF00423; HN; 1.				
SQ	SEQUENCE 577 AA; 63409 MW; DBBPF2CSEBIFDCCAD CRC64;				
	Query March	96.3%;	Score 2887;	DB 12;	Length 577;
	Best Local Similarity	95.8%;	Pred. No. 2.5e-228;		
	Matches 553; Conservative	10;	Mismatches 14;	Indels 0;	Gaps 0
OY	1 MDRASQVALENDEREAKTWRLIRIALTLTAVTVTIANSVASIVYSMGASTPSDLVGIP	60			
Dd	1 MDRAASQVALENDEREAKTWRLIRIALFLVTVTALISVASILYSKMASTPSDLVGIP	60			
Oy	61 TRISAERKITSLCSNDVDRIIKOVALESPLALINTETTIMAITSLSYOINGANN	120			

Dd	6I	TRISRAEKITSTGLSNDVDVRIKYQVALESPLALNTETTINMAITSLSIQINGAMANN	120
Oy	121	SGMGAPHDPFICGIGIKELLIVDNADSVTSFPYSAPOEHLNFI	180
Dd	121	SGMGAPHDPDPYICGIGIKELLYDDADSVTSFPYSAFOEHLNFI	180
Oy	181	SATHCYAHNYILSGCRDSSHSHOVLALGVLTARTTNGRFPSFTLASISLDDPNRSCSV	240
Dd	181	SATHCYAHNYILSGCRDSSHSHOVLPLGVLTARTSATGRVFFSTLSSINDDPNRSCSV	240
Oy	241	SATPLGCDMLCSKVETEEDEDYNSAFTLMAHGRIGFDQOHEKDLVTTLFEDWVANY	300
Dd	241	SATPLGCDMLCSKVETEEDEDYNSAVPTRMVHGRIGFDQOHEKDLVTTLFEDWVANY	300
Oy	301	GVGGGSSFDLGRVWVSVYGALKPNSSPDVVOESKXYIYKRYNTOCPDEODYOIRMAKSSYK	360
Dd	301	GVGGGSSFDLGRVWVSVYGALKPNSSPDVVOESKXYIYKRYNTOCPDEODYOIRMAKSSYK	360
Oy	361	PGREFGKRIQOAILISIKVSTSLGEBPVLTVPNTVTLMGABGRILVTGTSHEFLYORGSSY	420
Dd	361	PRRFGGKRRIQOAILISIKVSTSLGEBEPVLTVPNTVTLMGABGRILVTGTSHEFLYORGSSY	420
Oy	421	FSPALLVMTVTSNKTATLHSPYTPFAFFRRPGSIPCOASARCNSCVTYTDPYPLIFR	480
Dd	421	FSPALLVMTVTSNKTATLHSPYTPFAFFRRPGSIPCOASARCNSCVTYTDPYPLIFR	480
Oy	481	NHTLRGVGVTMLDSEQARLNPASAVFSDTSRSRITRVSSSTPKAAVTTSTCKRVVTKNT	540
Dd	481	NHTLRGVGVTMLDSEQARLNPASAVFSDTSRSRITRVSSSTPKAAVTTSTCKRVVTKNT	540
Oy	541	YCLSIATISNTLFGGFRIVPLVLVELLTKNDGVREANS	577
Dd	541	YCLSIATISNTLFGGFRIVPLVLVELLTKNDGVREANS	577

ID	Q9WCW3	PRELIMINARY;	PRT;	577 AA.
AC	Q9WCW3;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Hemagglutinin-neuraminidase (EC 3.2.1.18).			
GN	HN.			
OS	Newcastle disease virus.			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
OC	Paramyxoviridae; Paramyxovirinae; Rubulaviruses.			
OX	NCBI_TaxID=11176;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sagresta A., Villar E.;			
RL	Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF098289; AAD28331.1; -			
DR	InterPro; IPR000655; Hem-neuramndae.			
DR	Pfam; PF00423; HN; 1.			
DR	Glycosidase; Hydrolase.			
SQ	SEQUENCE 577 AA; 63347 MW; 5673484C1B9ECC7 CRC64;			
Query Match	96.3%; Score 2886; DB 12; Length 577;			
Best Local Similarity	96.4%; Pred. No. 3.1e-228;			
Matches 556; Conservative 8; Mismatches 13; Indels 0; Gaps 0				
Qy	1 MDRVSVQVLENDREAREAKTRRLIFRLILLLTVTTLTASVLSLYSMGASTPDLVGIP			60
Db	1 MDRVSVQVLENDREAREAKTRRLIFRLILFLTVTTTLTASVLSLYSMGASTPDLVGIP			60
Qy	61 TRIARAEEKITSALGSNODVVDRIYKVQVLESPLALNTETTINMAITSLSYQINGAANN			120
Db	61 TRIARAEEKITSLGSNODVVDRIYKVQVLESPLALNTETTINMAITSLSYQINGAANN			120
Qy	121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSYPSAFQEHNFIPAPTTGSGCTRIPSFDM			180
Db	121 SGWGAPIHDPDFYIGIGIKELIVDASDVTSYPSAFQEHNFIPAPTTGSGCTRIPSFDM			180

Qy	181	SATHYCYTHNVILISGGRDHSBHQVLAQVLTATTCGILFSTLRSLSDTQNRKCSV	240
Db	181	SATHYCYTHNVILISGGRDHSBHQVLAQVLTATTCGILFSTLRSLSDTQNRKCSV	240
Qy	241	SATPLGCDMLCSKVTEEBEEDYNASAVPTLMAHGRGFGQOQHEKDLVYTLFFEDMVANYP	300
Db	241	SATPLGCDMLCSKVTEEBEEDYNASAVPTLRMHGGIGFGQOQHEKDLVYTLFFGDMVANY	300
Qy	301	GVGGGSGFIDGRVWFSVYGGILKPNSPBDYVQEGKVIYKRYNDTCEDBDYQIRMAKSSYK	360
Db	301	LWVGSGFIDSRVWFSVYGGILKPNSPBDYVQEGKVIYKRYNDTCEDBDYQIRMAKSSYK	360
Qy	361	PGRFGGRIQOALLSLKUSTSLGDEPVLVPRNTYTLMAAGARILLYCTSHFLYQRRSSY	420
Db	361	PGRFGGRIQOALLSLKUSTSLGDEPVLVPRNTYTLMAAGARILLYGTSHFILYQRRSSY	420
Qy	421	FSRALLYPMTVSKNTATLHSPYTPNAFFRPGSIPQOASARCPNSCVGVYDPEPLFYR	480
Db	421	FSRALLYPMTVSKNTATLHSPYTPNAFFRPGSIPQOASARCPNSCVGVYDPEPLFYR	480
Qy	481	NHTLRGVFGTMDSEQARLNPASAVFDSITSRSRITRVSSSTKAAVYTTSTCFKVKVTKNTK	540
Db	481	NHTLRGVFGTMDGVQARLNPASAVFDSITSRSRITRVSSSTKAAVYTTSTCFKVKVTKNTK	540
Qy	541	YCSIAIEISNTLFGERRIYVPLVELLIKDDGVFEANSG	577
Db	541	YCSIAIEISNTLFGERRIYVPLVELLIKDDGVFEANSG	577

RESULT 14

ID	Q89712	PRELIMINARY;	PRT;	577	AA.
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DS HEMAGGLUTININ-neuraminidase.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VACCINE 6;
RX MEDLINE=96414821; PubMed=8817822;
RA Seal B.S., King D.J., Bennett J.D.;
RT "Characterization of Newcastle disease virus vaccines by biological
RT properties and sequence analysis of the hemagglutinin-neuraminidase
RT protein gene."
RL Vaccine 14:761-766(1996).
DR EMBL; U37192; AAC55046.1; -.
DR EMBL; U37189; AAC55043.1; -.
DR InterPro: IPR000665; Hem-neuraminidase.
DR Pfam; PF00423; HN; 1.
SQ SEQUENCE 577 AA; 63401 MW; 1BBB6ED5DEDC6C CRC64;

Query Match	95.5%;	Score 2863;	DB 12;	Length 577;
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Matches 550; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MDRVAVSQVALENDEREAKNTWRLIFRIAILLLTVTLATSVASLVSMGASTPSDLVGIP 60

Db 1 MDRVSVQVALENDEREAKNTWRLIFRIAILFLTVTTLAISVASLLYSMGASTPSDLVGIP 60

QY 61 TRISRAEKITSAŁGNOVDRIKKOVALESPŁALNTETTIMNAITSŁSYQINGAANN 120

Db 61 TRISRAEEKITSTLGSNDVDRIYKQVALESPALNTETTIMNAITSLSYQINGAANN 120

QY 121 SGWGAPIHDPDFIGGIGKELVDNASDVTSFYPSAQEHNLFIAPPTGSGCTRIPSDM 180

Db 121 SGWGAPIHDPDYIGGIGKELVDDASDVTSFYPSFQDHLNFIWAPTTRSGCTRIPSPDM 180

Qy	18	SATHCYCHTNVILSGCRDHSNHOVLGALVRTATAGIFPSTLRSLSDTDQNRKCSV	240
Db	181	SATHDCSHNVILSGCRDHSNHOVLGALVRTATAGFFPSTLRSLSDTDQNRKCSV	240
Qy	241	SATPLGCDMLCSKVTETEBEDYNASAVPTLMAHGRIGPDQYHEDLDVTLTFEDWVANYP	300
Db	241	SATPLGCDMLCSKVTETEBEDYNASAVPTLRVNHGRIGFDQYHEDLDVTLTFEDWVANYP	300
Qy	301	GVGGSFPIGRWFWFVYGGGLKPNSSSDVYQSGKYIYKRYNDTPEDDQYQIRMASSYK	360
Db	301	GVGGGSFIDSRWFWFVYGGGLKENTSPDVOEGKYIYKRYNDTPEDDQYQIRMAKSYK	360
Qy	361	PGRFGRKRIQOAILSTIKVSTSLGEBPVLTVPNTVTLMAAGAGRLITVGTSHFLYQRSSY	420
Db	361	PGRFGRKRIQOAILSTIKVSTSLGEBPVLTVPNTVTLMAAGAGRLITVGTSHFLYQRSSY	420
Qy	421	FSPALLYPMTVSNKRTATLHSPYTFNAFTRPESIPCOASARCPNSCVYVTDPPYLFIYR	480
Db	421	FSPALLYPMTVSNKRTATLHSPYTFNAFTRPESIPCOASARCPNSCVYVTDPPYLFIYR	480
Qy	481	NHTLRGVFGTMLDSEQARLNPAASAVFDSTSRITRIVSSSTKAAVYTTSTCFKVVTKNKT	540
Db	481	NHTLRGVFGTMLDSEQARLNPAASAVFDSTSRITRIVSPSSKAAVYTTSTCFKVVTKNKT	540
Qy	541	YCSIAIEISNTLFGFERIYVPLVLELTKNDGVRERASG	577
Db	541	YCSIAIEISNTLFGFERIYVPLVLELTKNDGVRERASG	577

RESULT 15

ID Q83843 PRELIMINARY; PRT; 577 AA.

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hemagglutinin-neuraminidase.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
OX NCBI_TaxID=11176;
RN [1]
RP
RP SEQUENCE FROM N.A.
RC STRAIN=vaccine 2;
RX MEDLINE=96414821; PubMed=8917822;
RA Seal B.S., King D.J., Bennett J.D.;
RT "Characterization of Newcastle disease virus vaccines by biological
RT properties and sequence analysis of the hemagglutinin-neuraminidase
RT protein gene."
RL Vaccine 14:761-766(1996).
RL EMBL, U37188; AAC55042.1. --
DR InterPro; IPR000665; Hem-neuramidae.
DR Pfam; PF00423; HN. 1.
SQ SEQUENCE 577 AA; 63174 MW; E3241EDB49B4CB33 CRC64;

Query Match	95.4%	Score 2860	DB 12	Length 577
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Matches 549; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 MDRVSVQVALENDEREAKNTWRLIFRIAILLLTVTLTATSVASLVSMGASTPSDLVGIP 60

Db 1 MDRAVSQVALENDEREA KNTWRLIFRIAILFLVTTLAISVASLLYSMGASTPSDLVGIP 60

61 TRISRAEKITSAŁGSNŌDVDRYKŌVALESPLALNTETTIMNAITSŁSYŌINGAANN 120

Db 61 TRISRAEKITSTLGSNDVDRIYKQVALESPLALLKTETTIMNAITSLSYQINGANN 120

QY 121 SGWGAPIHDPDFIGGIGKELIVDNASDVTSFYPSAQEHNLFIAPPTGSGCTRIPSDM 180

Db 121 RGMGAPIHDDPYIGGIGKELVDDASDVTSFYPSASQGQLNFIAPPTGSGCTRIPSFD 180

181 SATHYCYTHNVILSCGRDHS HQYLA GLVLR TATGRIFSTLSISLDDTONRKS CSV 240

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Db 181 SATQCYTHNVILSCCRDHSYQYISIGVLTSAIGRVFSTLRSINLDDTONKSCSV 240
Qy 241 SATPLGCDMLCSKYETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFEDWVANYP 300
Db 241 SATPLGCDMLCSKYETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFEDWVANYP 300
Qy 301 GVGGSFIDGRVWFSVYGLKPNPSDVOBGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
Db 301 GVGGSFIDSRVWFSYGLKPNPSDVOBGKYIYKRYNDTCPEBODYQIRMAKSSYK 360
Qy 361 PGRFGKRIOQAILISIKVSTSLGEDPVLTPPNTVTLMGAEGRILTVGSHFLYORGSSY 420
Db 361 PGRFGKRIOQAILISIKVSTSLGEDPVLTPPNTVTLMGAEGRILTVGSHFLYORGSSY 420
Qy 421 FSPALLYPMYVSNKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGVTDPYPLIFR 480
Db 421 FSPALLYPMYVSNKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGVTDPYPLIFR 480
Qy 481 NHTLRGVFGTMDSEQARLNPASAVFDSSTSRRTTRVSSSTKAAVTTSTCFKVKTKNT 540
Db 481 NHTLRGVFGTMDGVQARLNPASAVFDSSTSRRTTRVSSSTKAAVTTSTCFKVKTKNT 540
Qy 541 YCLSIABISNTLFGFRIVPLVETLKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFRIVPLVETLKNDGVREARSG 577

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 Job time : 67 secs

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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:51 ; Search time 18 Seconds
(without alignments)
1356.298 Million cell updates/sec

Title: US-09-915-515A-1

Perfect score: 2998
Sequence: 1 MDRVSOVALENDERAKNT.....IVPLVEIKNDVGREARSG 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PTUS COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2970	99.1	577	6 5310678-3	Patent No. 5310678
2	2920	97.4	577	1 US-07-820-154A-30	Sequence 30, Appl
3	2920	97.4	577	2 US-08-663-566A-11	Sequence 11, Appl
4	2920	97.4	577	2 US-08-097-554A-30	Sequence 30, Appl
5	2920	97.4	577	2 US-08-023-610-11	Sequence 11, Appl
6	2920	97.4	577	2 US-08-288-065A-11	Sequence 11, Appl
7	2920	97.4	577	2 US-08-362-240A-11	Sequence 11, Appl
8	2920	97.4	577	3 US-08-480-640A-30	Sequence 30, Appl
9	2920	97.4	577	3 US-08-295-802-30	Sequence 30, Appl
10	2920	97.4	577	3 US-08-804-372A-9	Sequence 9, Appl
11	2920	97.4	577	3 US-08-488-237A-30	Sequence 30, Appl
12	2920	97.4	577	4 US-08-375-992A-30	Sequence 30, Appl
13	2920	97.4	577	4 US-08-472-679H-30	Sequence 30, Appl
14	2920	97.4	577	5 PCT-US93-100324-30	Sequence 30, Appl
15	2920	97.4	577	5 PCT-US95-100245-11	Sequence 11, Appl
16	2915	97.2	581	2 US-08-484-575A-13	Sequence 13, Appl
17	2915	97.2	581	3 US-08-477-459-13	Sequence 13, Appl
18	2915	97.2	581	3 US-08-479-869-13	Sequence 13, Appl
19	2915	97.2	581	3 US-08-486-414-13	Sequence 13, Appl
20	2915	97.2	581	5 PCT-US94-01836A-13	Sequence 13, Appl
21	2915	97.2	581	5 PCT-US94-02252A-13	Sequence 13, Appl
22	2750	91.7	571	1 US-08-368-803-17	Sequence 17, Appl
23	2716.5	90.6	569	4 US-09-362-831-9	Sequence 9, Appl
24	765	25.5	565	2 US-08-700-548-2	Sequence 2, Appl
25	449	15.0	572	1 US-08-191-866D-81	Sequence 81, Appl
26	449	15.0	572	2 US-08-185-949B-81	Sequence 81, Appl
27	444.5	14.8	572	3 US-08-987-439-3	Sequence 3, Appl

28	442.5	14.8	572	2 US-08-467-963C-4	Sequence 4, Appl
29	442.5	14.8	572	2 US-08-838-189D-4	Sequence 4, Appl
30	442.5	14.8	572	3 US-08-852-344D-4	Sequence 4, Appl
31	442.5	14.8	572	3 US-08-344-639E-4	Sequence 4, Appl
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36	112	3.7	28	3 US-08-486-414-35	Sequence 35, Appl
37	102.5	3.4	1170	4 US-09-749-588-2	Sequence 2, Appl
38	101.5	3.4	1146	4 US-09-198-452A-580	Sequence 580, Appl
39	100.5	3.4	1752	4 US-09-865-621A-2	Sequence 2, Appl
40	99.5	3.3	650	3 US-08-362-525-2	Sequence 2, Appl
41	99	3.3	766	4 US-09-328-352-8230	Sequence 8230, Appl
42	97.5	3.3	804	4 US-09-328-352-5545	Sequence 5545, Appl
43	96	3.2	3892	4 US-09-328-352-5503	Sequence 5503, Appl
44	95.5	3.2	1584	3 US-09-251-645-6	Sequence 6, Appl
45	94	3.1	377	1 US-07-772-087-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1					
5310678-3					
Patent No. 5310678					
Applicant: Bingham, Richard W.; Chambers, Philip; Emerson, Peter					
T. Millar, Neil S.					
TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES					
NUMBER OF SEQUENCES: 3					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/07/438,945					
FILING DATE: 17-NOV-1989					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: 885,765					
FILING DATE: 15-JUL-1986					
SEQ ID NO:3:					
LENGTH:577					
5310678-3					
Query Match					
Best Local Similarity 99.1%; Score 2970; DB 6; Length 577;					
Pred. No. 3.2e-300;					
Matches 572; Conservative 2; Mismatches 3; Indels 0; Gaps 0;					
QY	1	MDRVSOVALENDERAKNTRLIFRIALLITVTATSVASIVSGASTBBDVICP	60		
DB	1	MDRVSOVALENDERAKNTWRLIFRIALLITVTATSVASIVSGASTBBDVICP	60		
QY	61	TRISRAEKTISALGSNOVDVDRILYKOVLESPLALNTETTINMAITSLSYQINGAANN	120		
DB	61	TRISRAEKTISALGSNOVDVDRILYKOVLESPLALNTETTINMAITSLSYQINGAANN	120		
QY	121	SGWGAIPHDPFIFGIGIKELIVDNASDVTSFYPBAFOEHLNFIAPPTGSGCTRI	180		
DB	121	SGWGAIPHDPFIFGIGIKELIVDNASDVTSFYPBAFOEHLNFIAPPTGSGCTRI	180		
QY	181	SATHYCTHNVITLGGCRDHSIOYALGVRTATGRIFPSTIRSLDPTORRKS	240		
DB	181	SATHYCTHNVITLGGCRDHSIOYALGVRTATGRIFPSTIRSLDPTORRKS	240		
QY	241	SATPLGCDMLCKSTETEEEDYNSAVPTLMAHGLGFDGOVHEKDLVTTLFEEDVANY	300		
DB	241	SATPLGCDMLCKSTETEEEDYNSAVPTLMAHGLGFDGOVHEKDLVTTLFEEDVANY	300		
QY	301	GVGGGSFIDGRVMSVYGLKPNPSPDVOEGKVIYIKRYNDPCPDQYQIRAKSKSYK	360		
DB	301	GVGGGSFIDGRVMSVYGLKPNPSPDVOEGKVIYIKRYNDPCPDQYQIRAKSKSYK	360		
QY	361	PGRRGKRIQOALISIVSISLSGDPVLTVPPNVTLMGAGRIILTYGTSIFLYORSSY	420		
DB	361	PGRRGKRIQOALISIVSISLSGDPVLTVPPNVTLMGAGRIILTYGTSIFLYORSSY	420		
QY	421	FSPALVPMVTSNKTATLHSPTFNATFRPSICQASARCPNSCVTVGVTDPPLFYR	480		

Db 421 FSPALLPYMTVSNKTKATLHSPYTFENAFTRPGSIPCOASARCPNSCVGYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEQARLNPAASVPDSTRSRITRVSSTKAAYTSTCFVVTNK 540
Db 481 NHTLRGVFGTMDSEQARLNPAASVPDSTRSRITRVSSTKAAYTSTCFVVTNK 540
QY 541 YCLSIASISNTLFGFRIPLVEILKNDGVRARSG 577
Db 541 YCLSIASISNTLFGFRIPLVEILKNDGVRARSG 577

RESULT 2
US-07-820-154A-30
Sequence 30, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David B
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820.154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELETEXT: 422523
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-30

Query Match 97.4%; Score 2920; DB 1; Length 577;
Best Local Similarity 96.9%; Pred. No. 5.1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 1 MDRASQVALENDERAKNTWRLIFRAILLLVVTATVASLVSMGASTPSDLVGP 60
Db 1 MDRASQVALENDERAKNTWRLIFRAILLLVVTATVASLVSMGASTPSDLVGP 60
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Db 61 TRISRAEKTTSALGSNOVDVRIYKQVALESPLALNTETIMNAITSLSYOINGANN 120
QY 121 SGSGAPRHHDDPFGIGIKELIVNADSVTSFYPSAPQEHNLFPAPPTGSGCTRIPEFDM 180
Db 121 SGSGAPRHHDDPFGIGIKELIVNADSVTSFYPSAPQEHNLFPAPPTGSGCTRIPEFDM 180
QY 181 SATHYCTYHNVILSGCRDHSYOLALGVLRATATGRIFPSTLSLSDTONRKSQSV 240
Db 181 SATHYCTYHNVILSGCRDHSYOLALGVLRATATGRIFPSTLSLSDTONRKSQSV 240
QY 241 SATPLGCDMLCSKTEETEEEDYNASVPTLMAHGRGLFGDQYHEKOLDVTTLFEDWVANY 300
Db 241 SATPLGCDMLCSKTEETEEEDYNASVPTLMAHGRGLFGDQYHEKOLDVTTLFEDWVANY 300

Db 241 SATPLGCDMLCSKATEETEEEDYNASVPTRMHGRGLFGDQYHEKOLDVTTLFEDWVANY 300
QY 301 GWGGGFFIDGRVWFVSYYGGLKPNSPEDTVQEGKVYIKAYNDPCPEODYQIRMAKSSYK 360
Db 301 GWGGGFFIDGRVWFVSYYGGLKPNSPEDTVQEGKVYIKAYNDPCPEODYQIRMAKSSYK 360
QY 361 PGRFGGKRIQQAILSIKVSISLGEEDPVLTPPVTYTLMAEGRIILTVGTSHPLYQSGSY 420
Db 361 PGRFGGKRIQQAILSIKVSISLGEEDPVLTPPVTYTLMAEGRIILTVGTSHPLYQSGSY 420
QY 421 FSPALLPYMTVSNKTKATLHSPYTFENAFTRPGSIPCOASARCPNSCVGYTDPYPLIFR 480
Db 421 FSPALLPYMTVSNKTKATLHSPYTFENAFTRPGSIPCOASARCPNSCVGYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEQARLNPAASVPDSTRSRITRVSSTKAAYTSTCFVVTNK 540
Db 481 NHTLRGVFGTMDSEQARLNPAASVPDSTRSRITRVSSTKAAYTSTCFVVTNK 540
QY 541 YCLSIASISNTLFGFRIPLVEILKNDGVRARSG 577
Db 541 YCLSIASISNTLFGFRIPLVEILKNDGVRARSG 577

RESULT 3
US-08-663-566A-11
Sequence 11, Application US/08663566A
Patent No. 5853733
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663.566A
FILING DATE: June 13, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28.678
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELETEXT: 422523
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-663-566A-11

Query Match 97.4%; Score 2920; DB 2; Length 577;
Best Local Similarity 96.9%; Pred. No. 5.1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 1 MDRASQVALENDERAKNTWRLIFRAILLLVVTATVASLVSMGASTPSDLVGP 60
Db 1 MDRASQVALENDERAKNTWRLIFRAILLLVVTATVASLVSMGASTPSDLVGP 60
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Db 61 TRISRAEKTTSALGSNOVDVRIYKQVALESPLALNTETIMNAITSLSYOINGANN 120

Db 61 TRISRAEEKITSTLGSNDQVVDRIYKQVLESPLALNTETTINMATTSLSYQINGANN 120
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Db 121 SGWGAPIHDDPFIIGIGIKELIVDNASDVTSFYPSAFOEHLNFIAPPTGGGCTRIPSFDM 180
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Db 181 SATHYCYTHNVILSGCRDHS HQYALGVLRRTATGRIFPSTLRSISLDDTONRKSCSV 240
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Db 241 SATPLGCDMLCSKATETEEDDYNASAVPTLMAHGLGPDQYHEKDLDTTLFEDMVANYP 300
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Db 301 GVGGGSFIDGRWVPSVYGLKPNPSPTVOEGKVIYKRYNDTCPEBDQYQIRMAKSSYK 360
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Db 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMAGGRLLVGTSHFLYQRGSSY 420
Qy 421 FSPALLYPMVTNSKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVGYTDPYPLIFYR 480
Db 421 FSPALLYPMVTNSKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVGYTDPYPLIFYR 480
Qy 481 NHTLRGVFTMLDSEORLNPAASVPDSTSRITRVSSTRAAYTSTCFKVKTKNT 540
Db 481 NHTLRGVFTMLDSEORLNPAASVPDSTSRITRVSSTRAAYTSTCFKVKTKNT 540
Qy 541 YCLSIABISNTLFGFRIPLVLEILKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFRIPLVLEILKNDGVREARSG 577

RESULT 4
US-08-097-554A-30
; Sequence 30, Application US/08097554A
; Patent No. 5869312
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; APPLICANT: Junker M.S., David E
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,554A
; FILING DATE: July 22, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 577 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-097-554A-30
Query Match 97.4%; Score 2920; DB 2; Length 577;
Best Local Similarity 96.9%; Pred. No. 5,1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MDRAVSQVALLENDERAKNTWRLIFRIAILLVTLATSVASIVYMGASTPSDLVGIP 60
Db 1 MDRAVSQVALLENDERAKNTWRLIFRIAILLVTLATSVASIVYMGASTPSDLVGIP 60
Qy 61 TRISRAEEKITSTLGSNDQVVDRIYKQVLESPLALNTETTINMATTSLSYQINGANN 120
Db 61 TRISRAEEKITSTLGSNDQVVDRIYKQVLESPLALNTETTINMATTSLSYQINGANN 120
Qy 121 SGWGAPIHDDPFIIGIGIKELIVDNASDVTSFYPSAFOEHLNFIAPPTGGGCTRIPSFDM 180
Db 121 SGWGAPIHDDPFIIGIGIKELIVDNASDVTSFYPSAFOEHLNFIAPPTGGGCTRIPSFDM 180
Qy 181 SATHYCYTHNVILSGCRDHS HQYALGVLRRTATGRIFPSTLRSISLDDTONRKSCSV 240
Db 181 SATHYCYTHNVILSGCRDHS HQYALGVLRRTATGRIFPSTLRSISLDDTONRKSCSV 240
Qy 241 SATPLGCDMLCSKATETEEDDYNASAVPTLMAHGLGPDQYHEKDLDTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKATETEEDDYNASAVPTLMAHGLGPDQYHEKDLDTTLFEDMVANYP 300
Qy 301 GVGGGSFIDGRWVPSVYGLKPNPSPTVOEGKVIYKRYNDTCPEBDQYQIRMAKSSYK 360
Db 301 GVGGGSFIDGRWVPSVYGLKPNPSPTVOEGKVIYKRYNDTCPEBDQYQIRMAKSSYK 360
Qy 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMAGGRLLVGTSHFLYQRGSSY 420
Db 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMAGGRLLVGTSHFLYQRGSSY 420
Qy 421 FSPALLYPMVTNSKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVGYTDPYPLIFYR 480
Db 421 FSPALLYPMVTNSKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVGYTDPYPLIFYR 480
Qy 481 NHTLRGVFTMLDSEORLNPAASVPDSTSRITRVSSTRAAYTSTCFKVKTKNT 540
Db 481 NHTLRGVFTMLDSEORLNPAASVPDSTSRITRVSSTRAAYTSTCFKVKTKNT 540
Qy 541 YCLSIABISNTLFGFRIPLVLEILKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFRIPLVLEILKNDGVREARSG 577

RESULT 5
US-08-023-610-11
; Sequence 11, Application US/08023610
; Patent No. 5926648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; APPLICANT: Macdonald Ph.D., Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-023-610-11

Query Match 97.4%; Score 2920; DB 2; Length 577;
Best Local Similarity 96.9%; Pred. No. 5.1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MDRAVQVLENDEREAKNTWRLIFRIAILLTVVTLATSVASLYSMGASTPSDLVGIP 60
DB 1 MDRAVQVLENDEREAKNTWRLIFRIAILLTVVTLATSVASLYSMGASTPSDLVGIP 60
QY 61 TRISRAEEKITSLAGSNQDVDRIRYQVVALESPLALINTEITIMATISLSYQINGAANN 120
DB 61 TRISRAEEKITSLAGSNQDVDRIRYQVVALESPLALINTEITIMATISLSYQINGAANN 120
QY 121 SGNGAPFIHDDPFIIGIGKELIVDNASDVTSFYPSAFOEHLNFIAPATTSGCTRIIPFDM 180
DB 121 SGNGAPFIHDDPFIIGIGKELIVDNASDVTSFYPSAFOEHLNFIAPATTSGCTRIIPFDM 180
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRITATGRIFESTLSISLDDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRITATGRIFESTLSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKATETEEEDYNSAVPTMAHGRGFDQYHEKDLDTTLFEDWVANYP 300
DB 241 SATPLGCDMLCSKATETEEEDYNSAVPTMAHGRGFDQYHEKDLDTTLFEDWVANYP 300
QY 301 GVGGSFIDGRWVFSYVGLKPNPSDPTVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360
DB 301 GVGGSFIDGRWVFSYVGLKPNPSDPTVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSIKSTSLGSDPVLTPPNTVTLMGAEGRLITVGTSHFLYQSGSSY 420
DB 361 PGRFGKRIQOAILSIKSTSLGSDPVLTPPNTVTLMGAEGRLITVGTSHFLYQSGSSY 420
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DB 421 FSPALLPYMTVSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTGYTDPYPLIFR 480
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DB 481 NHTLRGVFGTMDSEARLNPASAVPSTSRSTRIVSSSTKAAYTTSCTCFVVTNKNT 540
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DB 541 YCLSIASISNTLFGFRIIVPLVEILKNDGVREARSG 577
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RESULT 6
US-08-288-065A-11
Sequence 11, Application US/08288065A
Patent No. 5961982
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
TITLE OF INVENTION: HVT-050 and Uses Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,065A
FILING DATE: Aug-09-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-065A-11

Query Match 97.4%; Score 2920; DB 2; Length 577;
Best Local Similarity 96.9%; Pred. No. 5.1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MDRAVQVLENDEREAKNTWRLIFRIAILLTVVTLATSVASLYSMGASTPSDLVGIP 60
DB 1 MDRAVQVLENDEREAKNTWRLIFRIAILLTVVTLATSVASLYSMGASTPSDLVGIP 60
QY 61 TRISRAEEKITSLAGSNQDVDRIRYQVVALESPLALINTEITIMATISLSYQINGAANN 120
DB 61 TRISRAEEKITSLAGSNQDVDRIRYQVVALESPLALINTEITIMATISLSYQINGAANN 120
QY 121 SGNGAPFIHDDPFIIGIGKELIVDNASDVTSFYPSAFOEHLNFIAPATTSGCTRIIPFDM 180
DB 121 SGNGAPFIHDDPFIIGIGKELIVDNASDVTSFYPSAFOEHLNFIAPATTSGCTRIIPFDM 180
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRITATGRIFESTLSISLDDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRITATGRIFESTLSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKATETEEEDYNSAVPTMAHGRGFDQYHEKDLDTTLFEDWVANYP 300
DB 241 SATPLGCDMLCSKATETEEEDYNSAVPTMAHGRGFDQYHEKDLDTTLFEDWVANYP 300
QY 301 GVGGSFIDGRWVFSYVGLKPNPSDPTVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360
DB 301 GVGGSFIDGRWVFSYVGLKPNPSDPTVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSIKSTSLGSDPVLTPPNTVTLMGAEGRLITVGTSHFLYQSGSSY 420
DB 361 PGRFGKRIQOAILSIKSTSLGSDPVLTPPNTVTLMGAEGRLITVGTSHFLYQSGSSY 420
QY 421 FSPALLPYMTVSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTGYTDPYPLIFR 480
DB 421 FSPALLPYMTVSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTGYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEARLNPASAVPSTSRSTRIVSSSTKAAYTTSCTCFVVTNKNT 540
DB 481 NHTLRGVFGTMDSEARLNPASAVPSTSRSTRIVSSSTKAAYTTSCTCFVVTNKNT 540
QY 541 YCLSIASISNTLFGFRIIVPLVEILKNDGVREARSG 577
DB 541 YCLSIASISNTLFGFRIIVPLVEILKNDGVREARSG 577
```

RESULT 7
US-08-362-240A-11

Sequence 11, Application US/08362240A
Patent No. 5965138
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Junker, David
APPLICANT: Wild, Martha A
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,240A
FILING DATE: Dec-22-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-240A-11

Query Match 97.4%; Score 2920; DB 2; Length 577;
Best Local Similarity 96.9%; Pred. No. 5.1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRVSVQALNDREAEKNTWRLIFRIALLTVTLATSVASLYSMGASTPSDLVIGIP 60
DB 1 MDRVSVQALNDREAEKNTWRLIFRIALLTVTLATSVASLYSMGASTPSDLVIGIP 60
QY 61 TRISRAEKITSAAGSNQDVVDRIYKQVLESPLALNTETTINMAITSLSYQINGANN 120
DB 61 TRISRAEKITSAAGSNQDVVDRIYKQVLESPLALNTETTINMAITSLSYQINGANN 120
QY 121 SGWAPTHDPDFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
DB 121 SGWAPTHDPDFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
QY 121 SATHYCYTHNVILSGCRDHS HQYLAVGLRTATGRIFPSTLRSLDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLAVGLRTATGRIFPSTLRSLDTONRKSCSV 240
QY 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQGYHEKDLVTTLFGDWVANYP 300
DB 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQGYHEKDLVTTLFGDWVANYP 300
QY 301 GVGGSFIDGWSVSVYGLKPNPSDVTVOGKVIYIRYNDTCPEDEDDYQIRAKKSYK 360
DB 301 GVGGSFIDGWSVSVYGLKPNPSDVTVOGKVIYIRYNDTCPEDEDDYQIRAKKSYK 360
QY 361 PGRFGKRIQQAIIISIKVSTSLGSDPVLTVPNTYTLMAEGRIITVGTSHFLVORGSSY 420
DB 361 PGRFGKRIQQAIIISIKVSTSLGSDPVLTVPNTYTLMAEGRIITVGTSHFLVORGSSY 420
QY 421 FSPALLYPMVTSNKTALHSPYTFNAFTPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
DB 421 FSPALLYPMVTSNKTALHSPYTFNAFTPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480

DB 421 FSPALLYPMVTSNKTALHSPYTFNAFTPGSIPCOASARCPNSCVTVGYTDPYPLIFYR 480
QY 481 NHTLRGVFGTMDSEQARLNPASAVPSTSRRTTRYSSTSKAAYTSTCFKVKTKNT 540
DB 481 NHTLRGVFGTMDSEQARLNPASAVPSTSRRTTRYSSTSKAAYTSTCFKVKTKNT 540
QY 541 YCLISIAEISNTLFGFEPRIVPLVLEILKNDGVREARSG 577
DB 541 YCLISIAEISNTLFGFEPRIVPLVLEILKNDGVREARSG 577

RESULT 8
US-08-480-640A-30
Sequence 30, Application US/08480640A
Patent No. 6033904
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,640A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-640A-30

Query Match 97.4%; Score 2920; DB 3; Length 577;
Best Local Similarity 96.9%; Pred. No. 5.1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRVSVQALNDREAEKNTWRLIFRIALLTVTLATSVASLYSMGASTPSDLVIGIP 60
DB 1 MDRVSVQALNDREAEKNTWRLIFRIALLTVTLATSVASLYSMGASTPSDLVIGIP 60
QY 61 TRISRAEKITSAAGSNQDVVDRIYKQVLESPLALNTETTINMAITSLSYQINGANN 120
DB 61 TRISRAEKITSAAGSNQDVVDRIYKQVLESPLALNTETTINMAITSLSYQINGANN 120
QY 121 SGWAPTHDPDFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
DB 121 SGWAPTHDPDFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180
QY 181 SATHYCYTHNVILSGCRDHS HQYLAVGLRTATGRIFPSTLRSLDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLAVGLRTATGRIFPSTLRSLDTONRKSCSV 240
QY 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQGYHEKDLVTTLFGDWVANYP 300
DB 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQGYHEKDLVTTLFGDWVANYP 300

Qy	30L	GWGGSEFIDGRVWFVSFYGGGLKXNSSDPVYQSGKYIYKRNYDTCPEBODYQIMAASSYK	360
Db	30I	GWGGSEFIDSRVWFVSFYGGGLKKNPNTSDVYQSGKIYKRYNDTCPEBDYQIMAASSYK	360
Qy	36I	PGAFGSKRIQAAILSLIKYSTSLGEEDPVLTVPNPTVTLMGAERILLTVGTSHFLYQRGSY	420
Db	36I	PGFEGSKRIQAAILSLIKYSTSLGEEDPVLTVPNPTVTLMGAERILLTVGTSHFLYQRGSY	420
Qy	42I	FSPALLPYMTVASNKRTATLSPTYFNAPFRPGSIPCOASARCPNSCVGYTDPPLIFR	480
Db	42I	FSPALLPYMTVASNKRTATLSPTYFNAPFRPGSIPCOASARCPNSCVGYTDPPLIFR	480
Qy	48I	NHTLRGVFGTMLDSEQARLNPAASAVIDSTSRSRITRVSSSTKAAYTTSTCFPKVKTNKT	540
Db	48I	NHTLRGVFGTMLDSEQARLNPAASAVIDSTSRSRITRVSSSIKAAYYTTSTCFPKVKTNKT	540
Qy	54I	YCISIAEISNTLFGPRIRIVLLVELLINDGVREARSG	577
Db	54I	YCISIAEISNTLFGPRIRIVLLVELLKDDGVREARSG	577

RESULT 9

US-08-295-802-30
Sequence 30, Application US/08295802
Patent No. 6127163
GENERAL INFORMATION:
APPLICANT: Cochran Ph. D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 188
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentm Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,802
FILING DATE: Herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-295-802-30

Query Match 97.4%; Score 2920; DB 3; Length 577;

Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

OV 1 MPRAVSOVALENDEREAKNTWRIETRIAILLTVTITATSVASLVYSGASTPSDLYGIP 60

1 MBRAYSOVAL ENDEBEAKNTWPI TERIATI EL TVVETI AISVASI I YSMGASTPSDI VGTB 60

03: C1 PBTGDBFEKTCATCCNNDYHDTVKOUAYECNRATTWHTTETMOJLTPCQAVOTWCAHHY 100

QY 121 SGWCAPIHDPDFIGIGKELIVNASDVTSFYPSAQEHLNFIAPPTGGCTRIPSPFM 180

D6 121 SGWGAPIHDPDYIGGIGKELI VDDASDVTSFYPSAFQEHNLNFI PAPTIGSGCTIRIPSFDM 180

181 SATHYCYTHNVILSGCRDHS HQYLALGVLR TATGRIFFSTLSISLDDTQNRKSCSV 240

Db 181 SATHYCYTHNVILSGCRDHS SHQYLA LGVLRTSATGRVFFSTLSINLDDTQNRKSCSV 240

QY 241 SATPLGCDMLCSKVTEETEEDYNSAVPTLMAHGRLGFDGQYHEKDLVTTLFEDWVANYP 300

Db 241 SATPLGCDMLCSKATETEEEDYNSAVPTRMVHGRIGFDGQYHEKDLDTTLFGDWVANYR 300

301 GVGGSFIDGRWFESVYGG LKPNSPSDTVOEGKV IYKRNDTCPD EODYOIRMAKSSYK 360

301 CVCGSPIDSPVWSEVYCGI.KPNTBPSDTVOEGKYLYKPYNDTCPENDYQIRMAKSSYK 360

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DB 421 FSEALDIFMIVSNKIAIHNSFI IFNFI IFGSI FCYASAKCFNSCVIGVIAIDFIEPIFIK 400

481 NHTLRGVFGTMLDSEQARLNPASAVFDTSRSRITRVSSSSIKAYITISICFKVVKINKT 540

Db 481 NHTLRGVFGTMDGEQARLNPAASAVFDSTSRSRITRVSSSSIKAAYYTSTCFKVKTKNKT 540

QY 541 YCLSLAISNTLFGFRIVPLVEILKNDGVREARSG 577

Db 541 YCLSLAIEISNTLGEFRIVPLLVEILKDDGVREARSG 577

RESULT 10

US-08-804-372A-9
Sequence 9, Application US/08804372A
Patent No. 6183753
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Wild, Martha A.
APPLICANT: Winslow, Barbara J.
TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,372A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2552/39115E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,992A
FILING DATE: Herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-375-992A-30

Query Match 97.4%; Score 2920; DB 4; Length 577;
Best Local Similarity 96.9%; Pred. No. 5,1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MRAVSOVLENDREKAKTWRILFRIALLTVTLATSVASLYSMGASTPSDVGIP 60
DB 1 MRAVSOVLENDREKAKTWRILFRIALLTVTLATSVASLYSMGASTPSDVGIP 60
QY 61 TRISRAEEKITSLGSGNOVDRIYKQVLESPLALNTETIMNATSLSYQINGAAN 120
DB 61 TRISRAEEKITSLGSGNOVDRIYKQVLESPLALNTETIMNATSLSYQINGAAN 120
QY 121 SGWGAPIHDPDFIGIGKELIVDNASDVTSFYPSAQEHLNFIPTTSGGCTRIPSFDM 180
DB 121 SGWGAPIHDPDFIGIGKELIVDNASDVTSFYPSAQEHLNFIPTTSGGCTRIPSFDM 180
QY 181 SATHYCTYTHNVILSGCRDHS HQYLALGVLTATGRIFESTLSISLDTQNRKSCSV 240
DB 181 SATHYCTYTHNVILSGCRDHS HQYLALGVLTATGRIFESTLSISLDTQNRKSCSV 240
QY 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFEDWYANP 300
DB 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFEDWYANP 300
QY 301 GVGGGSFIDGRVWFSVYGGAKPNSPDTVOEGKVIYKRYNDTCPEQDYQIRMAKSSYK 360
DB 301 GVGGGSFIDGRVWFSVYGGAKPNSPDTVOEGKVIYKRYNDTCPEQDYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSIKYSTSLGDEPVLTPPNTVTLMAGRILTVGTSHPLYQSGSSY 420
DB 361 PGRFGKRIQOAILSIKYSTSLGDEPVLTPPNTVTLMAGRILTVGTSHPLYQSGSSY 420
QY 421 FSPALLYPMVTGSKTATLTHSPYTFNAFTPGSIPCOASARCPNSCVGYTDPYPLIFR 480
DB 421 FSPALLYPMVTGSKTATLTHSPYTFNAFTPGSIPCOASARCPNSCVGYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSTRITRVSSSTKAAYTSTCFKVVTKNTK 540
DB 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSTRITRVSSSTKAAYTSTCFKVVTKNTK 540
QY 541 YCLSIASISNTLFGEPRIIVPLVLEILKNDGVREARS 577
DB 541 YCLSIASISNTLFGEPRIIVPLVLEILKNDGVREARS 577

RESULT 13
US-08-472-679H-30
Sequence 30, Application US/08472679H
Patent No. 6497882

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.
Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESS: Pamela G. Salkeid
STREET: 2000 Galloping Hill Road
CITY: New Jersey
STATE: New Jersey
COUNTRY: USA

ZIP: 07033

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/472,679H

FILING DATE: 07-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Salkeid, Pamela G.

REGISTRATION NUMBER: 38,607

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 298-2135

TELEFAX: (908) 298-5388

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 577 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-08-472-679H-30

Query Match 97.4%; Score 2920; DB 4; Length 577;
Best Local Similarity 96.9%; Pred. No. 5,1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MRAVSOVLENDREKAKTWRILFRIALLTVTLATSVASLYSMGASTPSDVGIP 60
DB 1 MRAVSOVLENDREKAKTWRILFRIALLTVTLATSVASLYSMGASTPSDVGIP 60
QY 61 TRISRAEEKITSLGSGNOVDRIYKQVLESPLALNTETIMNATSLSYQINGAAN 120
DB 61 TRISRAEEKITSLGSGNOVDRIYKQVLESPLALNTETIMNATSLSYQINGAAN 120
QY 121 SGWGAPIHDPDFIGIGKELIVDNASDVTSFYPSAQEHLNFIPTTSGGCTRIPSFDM 180
DB 121 SGWGAPIHDPDFIGIGKELIVDNASDVTSFYPSAQEHLNFIPTTSGGCTRIPSFDM 180
QY 181 SATHYCTYTHNVILSGCRDHS HQYLALGVLTATGRIFESTLSISLDTQNRKSCSV 240
DB 181 SATHYCTYTHNVILSGCRDHS HQYLALGVLTATGRIFESTLSISLDTQNRKSCSV 240
QY 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFEDWYANP 300
DB 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFEDWYANP 300
QY 301 GVGGGSFIDGRVWFSVYGGAKPNSPDTVOEGKVIYKRYNDTCPEQDYQIRMAKSSYK 360
DB 301 GVGGGSFIDGRVWFSVYGGAKPNSPDTVOEGKVIYKRYNDTCPEQDYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSIKYSTSLGDEPVLTPPNTVTLMAGRILTVGTSHPLYQSGSSY 420
DB 361 PGRFGKRIQOAILSIKYSTSLGDEPVLTPPNTVTLMAGRILTVGTSHPLYQSGSSY 420
QY 421 FSPALLYPMVTGSKTATLTHSPYTFNAFTPGSIPCOASARCPNSCVGYTDPYPLIFR 480
DB 421 FSPALLYPMVTGSKTATLTHSPYTFNAFTPGSIPCOASARCPNSCVGYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSTRITRVSSSTKAAYTSTCFKVVTKNTK 540
DB 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSTRITRVSSSTKAAYTSTCFKVVTKNTK 540

|||||
Db 481 NHTLRGVGTMDEQARLNPASAVFDSSTSRITRVSSSIKAYTSTCFKVKTKNT 540
QY 541 YCLSIABISNTLFGFRIVPLVEILLKNDGVEARSG 577
Db 541 YCLSIABISNTLFGFRIVPLVEILLKNDGVEARSG 577

RESULT 14

PCT-US93-00324-30
Sequence 30, Application PC/TUS9300324
GENERAL INFORMATION:
APPLICANT: Cochran Ph. D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00324
FILING DATE: 19930113
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-00324-30

Query Match 97.4%; Score 2920; DB 5; Length 577;
Best Local Similarity 96.9%; Pred. No. 5.1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRASQVLENDREAKNTWRLIFRIAILLTAVTLATSVASLVYMGASTPSPDLVGP 60
Db 1 MDRASQVLENDREAKNTWRLIFRIAILLTAVTLATSVASLVYMGASTPSPDLVGP 60
QY 61 TRISRAEKITSTLGSNODVDRIYKQVLESPLALNTETTTINNAITSLSYQINGAAN 120
Db 61 TRISRAEKITSTLGSNODVDRIYKQVLESPLALNTETTTINNAITSLSYQINGAAN 120
QY 121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIIPFDM 180
Db 121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIIPFDM 180
QY 181 SATHYCTHNVILSGCRDHS HQYLAVLRTATGRIFFSTLRSISLDTQNRKSCSV 240
Db 181 SATHYCTHNVILSGCRDHS HQYLAVLRTATGRIFFSTLRSISLDTQNRKSCSV 240
QY 241 SATPLGCDMLCSKYETEEDYNSAVPTLMAHGRGFGQYHEKDLDTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYETEEDYNSAVPTLMAHGRGFGQYHEKDLDTTLFEDMVANYP 300
QY 301 GVGGSFIDGKVPWSVYGLKPNPSDTVOEGKYVIYRRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSFIDGKVPWSVYGLKPNPSDTVOEGKYVIYRRYNDTCPEODYQIRMAKSSYK 360

QY 361 GPRFGRIQQAIIISIVSTSLGEDPVLVTPNTVTLMAGRIITVGTSHFLYQRGSSY 420
Db 361 GPRFGRIQQAIIISIVSTSLGEDPVLVTPNTVTLMAGRIITVGTSHFLYQRGSSY 420
QY 421 FSPALYPMVTSNKTATLHSPYFNATFRPGSIPQASARCPNSCVTVTDYPPLIFYR 480
Db 421 FSPALYPMVTSNKTATLHSPYFNATFRPGSIPQASARCPNSCVTVTDYPPLIFYR 480
QY 481 NHTLRGVGTMDEQARLNPASAVFDSSTSRITRVSSSTKAYTSTCFKVKTKNT 540
Db 481 NHTLRGVGTMDEQARLNPASAVFDSSTSRITRVSSSTKAYTSTCFKVKTKNT 540
QY 541 YCLSIABISNTLFGFRIVPLVEILLKNDGVEARSG 577
Db 541 YCLSIABISNTLFGFRIVPLVEILLKNDGVEARSG 577

RESULT 15

PCT-US95-10245-11
Sequence 11, Application PC/TUS9510245
GENERAL INFORMATION:
APPLICANT: SYNTRO CORPORATION
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10245
FILING DATE: 09-AUG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-10245-11

Query Match 97.4%; Score 2920; DB 5; Length 577;
Best Local Similarity 96.9%; Pred. No. 5.1e-295;
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRASQVLENDREAKNTWRLIFRIAILLTAVTLATSVASLVYMGASTPSPDLVGP 60
Db 1 MDRASQVLENDREAKNTWRLIFRIAILLTAVTLATSVASLVYMGASTPSPDLVGP 60
QY 61 TRISRAEKITSTLGSNODVDRIYKQVLESPLALNTETTTINNAITSLSYQINGAAN 120
Db 61 TRISRAEKITSTLGSNODVDRIYKQVLESPLALNTETTTINNAITSLSYQINGAAN 120
QY 121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIIPFDM 180
Db 121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIIPFDM 180
QY 181 SATHYCTHNVILSGCRDHS HQYLAVLRTATGRIFFSTLRSISLDTQNRKSCSV 240
Db 181 SATHYCTHNVILSGCRDHS HQYLAVLRTATGRIFFSTLRSISLDTQNRKSCSV 240

Db 181 SATHYCTHNVIIISGCRDHSHQYLAGVLRISATGRVFFSTLRSINLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKVTETEEEDYNASAVPTLMAHGRIAGFDQYHEKDLVTTLPEDWVANYP 300
Db 241 SATPLGCDMLCSKVTETEEEDYNASAVPTLMAHGRIAGFDQYHEKDLVTTLPEDWVANYP 300
QY 301 GVGGSFIDGRVWFSVYGLKPNSPSDTVQEGKVIYKRYNDTCPEQDYQIRMAKSSYK 360
Db 301 GVGGSFIDGRVWFSVYGLKPNSPSDTVQEGKVIYKRYNDTCPEQDYQIRMAKSSYK 360
QY 361 PGRFGGRRIQOAILISTVSTSLGSDPVLTPPNTVTLMGAEGRILTVGISHFLYORGSSY 420
Db 361 PGRFGGRRIQOAILISTVSTSLGSDPVLTPPNTVTLMGAEGRILTVGISHFLYORGSSY 420
QY 421 FSPALLVPMVSNKATLHSPYTFENAFTRPGSIPCOASARCPNSCVTGVYTDPPYPLIFYR 480
Db 421 FSPALLVPMVSNKATLHSPYTFENAFTRPGSIPCOASARCPNSCVTGVYTDPPYPLIFYR 480
QY 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSSSTKAAVTTSTCFKVKTKNTK 540
Db 481 NHTLRGVFGTMDSEQARLNPASAVPDSRSRITRVSSSSSTKAAVTTSTCFKVKTKNTK 540
QY 541 YCLSIABISNTLFGFRIVPLVLEILKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFRIVPLVLEILKNDGVREARSG 577

Search completed: January 2, 2004, 16:17:21
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:18:56 ; Search time 51 Seconds
(without alignments)
2270.000 Million cell updates/sec

Title: US-09-915-515A-1

Perfect score: 2998
Sequence: 1 MDRVSOVALENDREANKNT.....IVPLLVELLKNDGVREARSG 577

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2998	100.0	577	9	US-09-915-515A-1
2	446	14.9	575	12	US-10-226-629A-17
3	145	4.8	1723	9	US-09-841-132-395
4	144	4.0	1723	9	US-09-841-132-394
5	119	4.0	1198	11	US-09-975-719-405
6	116	3.9	2283	12	US-10-172-502-4
7	114	3.8	5877	15	US-10-142-515-11
8	114	3.8	5935	15	US-10-243-243A-8
9	112.5	3.8	2344	9	US-09-815-242-12713
10	111	3.7	9799	12	US-09-965-738-146
11	111	3.7	11721	12	US-09-965-738-162
12	108.5	3.7	1510	10	US-09-738-626-3707
13	108	3.6	1609	12	US-10-369-493-1535
14	108	3.6	5636	12	US-10-032-189-128
15	108	3.6	5636	12	US-10-120-801-72

16	108	3.6	5636	12	US-10-023-634-93	Sequence 93, App1
17	106.5	3.6	1500	10	US-09-870-759-136	Sequence 136, App
18	106.5	3.6	1500	12	US-09-751-708A-136	Sequence 136, App
19	105.5	3.5	590	12	US-10-403-337-70	Sequence 70, App1
20	104.5	3.5	650	12	US-10-369-493-22177	Sequence 22177, A
21	104.5	3.5	689	15	US-10-202-846-2-6732	Sequence 2, App11
22	104	3.5	1367	12	US-10-369-493-16732	Sequence 16732, A
23	102.5	3.4	1170	14	US-10-135-687-2	Sequence 2, App11
24	102.5	3.4	1210	10	US-09-660-352A-2	Sequence 2, App11
25	100.5	3.4	1752	12	US-10-387-388-2	Sequence 2, App11
26	100	3.3	345	10	US-09-738-626-6698	Sequence 6698, Ap
27	100	3.3	1316	12	US-10-028-248A-48	Sequence 48, App1
28	100	3.3	1797	12	US-10-369-493-5176	Sequence 5176, Ap
29	100	3.3	1805	12	US-10-369-493-5177	Sequence 5177, Ap
30	98	3.3	1160	12	US-10-115-482-46	Sequence 46, App1
31	98	3.3	1842	12	US-10-369-493-2225	Sequence 2225, Ap
32	97.5	3.3	834	12	US-10-094-749-2227	Sequence 2227, Ap
33	97.5	3.3	1082	12	US-10-369-493-17890	Sequence 17890, A
34	96.5	3.2	660	15	US-10-128-714-3291	Sequence 3291, Ap
35	96.5	3.2	794	15	US-10-128-714-8291	Sequence 8291, Ap
36	96.5	3.2	1659	10	US-09-801-368-118	Sequence 118, App
37	96	3.2	557	11	US-09-934-455-326	Sequence 326, App
38	96	3.2	557	12	US-10-302-267-198	Sequence 198, App
39	96	3.2	1075	10	US-09-801-368-110	Sequence 110, App
40	96	3.2	1075	12	US-10-369-493-22068	Sequence 22068, A
41	96	3.2	1110	15	US-10-149-819-12	Sequence 12, App1
42	96	3.2	1666	15	US-10-128-714-3553	Sequence 3553, Ap
43	96	3.2	1680	15	US-10-128-714-8553	Sequence 8553, Ap
44	96	3.2	1751	9	US-09-841-132-445	Sequence 445, App
45	96	3.2	1751	9	US-09-841-132-594	Sequence 594, App

ALIGNMENTS

RESULT 1
US-09-915-515A-1
; Sequence 1, Application US/0915515A
; Patent No. US20020081572A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Gary
; APPLICANT: Portner, Allen
; APPLICANT: Takimoto, Toru
; APPLICANT: Babu, Y. Sudhakar
; APPLICANT: Rowland, R. Scott
; TITLE OF INVENTION: three Dimensional Structure of Paramyxovirus Hemagglutinin-Neurami
; FILE REFERENCE: 1663/00142
; CURRENT APPLICATION NUMBER: US/09/915, 515A
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Newcastle Disease Virus (Kansas Strain)
US-09-915-515A-1

Query Match 100.0%; Score 2998; DB 9; Length 577;
Best Local Similarity 100.0%; Pred. No. 7e-289;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDRAVSQVALENDREANKNTWRLIFRIAILLVTTLTATSVASLVYSGASTPDDIVIP	60
DB	1	MDRAVSQVALENDREANKNTWRLIFRIAILLVTTLTATSVASLVYSGASTPDDIVIP	60
QY	61	TRISRAEKITSALGSNDVDVRIYKOVLESPLALNTETFINNAITSLSYQINGANN	120
DB	61	TRISRAEKITSALGSNDVDVRIYKOVLESPLALNTETFINNAITSLSYQINGANN	120
QY	121	SGKAPIHDPFIFGIGKELIVDNASDVTSFYPSAFQHLNFIPAPTTGSGCTRIPSFDM	180
DB	121	SGKAPIHDPFIFGIGKELIVDNASDVTSFYPSAFQHLNFIPAPTTGSGCTRIPSFDM	180

QY	181	SATYCVYHANYILSCCRSHSHSHOYLAAGVLRRTYTGILPSTLSRLSDTQNRKSCSV	240
Db	181	SATYCYTHANYILSCCRSHSHSHOYLAAGVLRRTYTGILPSTLSRLSDTQNRKSCSV	240
QY	241	SATPLGCDMLCSKYLETEEEDYNSAVPTLMAHGRIGFDQYHEKDLDVTLTFEEDWVANYP	300
Db	241	SATPLGCDMLCSKYLETEEEDYNSAVPTLMAHGRIGFDQYHEKDLDVTLTFEEDWVANYP	300
QY	301	GVGGGSFLDGVWVSVYVGLKPNSPSDTVQSGKYVYTKRYNDTCPEDEDYQIRNAKSSYK	360
Db	301	GVGGGSFLDGVWVSFVSYVGLKPNSPSDTVQSGKYVYTKRYNDTCPEDEDYQIRNAKSSYK	360
QY	361	PGRGGRKIQOALLISIKVSTSLGSDPYLTVENPTVTLMAGARGLITVGTSHFLVORGSSY	420
Db	361	PGRGGRKIQOALLISIKVSTSLGSDPYLTVENPTVTLMAGARGLITVGTSHFLVORGSSY	420
QY	421	FSPALLVPMYTSNKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVGVTDPYPLIYR	480
Db	421	FSPALLVPMYTSNKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVGVTDPYPLIYR	480
QY	481	NHTLRGVFGTMLDSEQARLNPASAVFDSSTSRITRVSSSTKAYTTSCTCFKXVKTKNT	540
Db	481	NHTLRGVFGTMLDSEQARLNPASAVFDSSTSRITRVSSSTKAYTTSCTCFKXVKTKNT	540
QY	541	YCSIAETSNLTFGEFRIVPLLVETLKNQDGVREARSG	577
Db	541	YCSIAETSNLTFGEFRIVPLLVETLKNQDGVREARSG	577

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RESULT 2
US-10-226-629A-17
; Sequence 17, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitx, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226.629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Human parainfluenza virus 1
; US-10-226-629A-17

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	Query March	14.9%	Score 446;	DB 12;	Length 575;
	Best Local Similarity	27.5%;	Pred. No. 5.2e-35;		
	Matches 155;	Conservative 92;	Mismatches 237;	Indels 80;	Gaps 20;
QY	26 RIALLLTVTLATLSVA-----SLVSYSGASTPSDVLGIPRISRA--EERKITSAL	74			
	: : : : : : : : : :				
Db	32 RIHIMLIATTMTHTLVSFTIIMILCIDILLIKODTCWKITMIVSSMNESAKTIKETITELI	91			
QY	75 GSNDDVDVR-LYKKOVALSEPL-ALLNTEETITMAITSLSYGINGAANNSSGCAGPIHDPDF	132			
	: : : : : : : : : : : : : : : :				
Db	92 --ROEVISRTINIOSSVOSGIPIILINKOSRDLTOIEKSCROELAOICENTTIIHHADG	149			
QY	133 IG-----GIQKELEIVDNASDVTSFYSPAEQHILNFIPAP-----TTGSGCTRIIP	176			
	: : : : : : : : : : : : : : : :				
Db	150 ISPLDPDHFWRCAPGEPLLSNN-----PNISLLPGSLLSGSTTIGCVRLP	196			
QY	177 SFPMDSATHYCTHNVLISGCRDHSHTOYLATGVLTARTAGRIFFTSLRSLSDLTQNRR	236			
	: : : : : : : : : : : : : : : :				
Db	197 SLISGDALIVASSNLITGGCADIGKSIVOVLDTGISLNSDMYPDLNPVTISHTYINDNRK	256			
QY	237 SCGSVASATPLGCDMLCSKVETEEDDYNSAVPTLNAHGRLGFDG----QYHEKDIDVTTL	291			

[illegible]

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RESULT 3
US-09-841-132-395
Sequence 395, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841.132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ. ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 395
LENGTH: 1723
TYPE: PR1
ORGANISM: Chlamydia pneumoniae
US-09-841-132-395

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Query Match 4.8%; Score 145; DB 9; Length 1723;
Best Local Similarity 18.8%; Pred. No. 0.00028;
Matches 141; Conservative 88; Mismatches 284; Indels 236; Gaps 29

Qy      4 AVSQALEN--DEREAKTWR-----LIFRIALLTVVLATSVASLVSMG 49
Db      449 AVGQVLTLEIDIANLKNMTNNCKGEGAIYTKKALITNGGALLTPSGTSTDNGCALFVG 508

Qy      50 AASPDLVGI---PRISPAEEKITSALGNOQDVVDRIYQVALESPL----- 94
Db      509 GILSLDLVEVRSEKKNKTGYSAPITKASNTAPVVS--SSTMASEPVAAPAAAAEVTA 565

Qy      95 ----ALNMTETINNAITSLYQINGANNNGWKAPI-----HDPDFI----- 133
Db      566 AKGAGALYSTEGLTVGIGTISILSFENNCCONOGGAYVTKTQCSDSHRLFTSNKAADG 625

Qy      134 GGI--GKEILVNMAADVTSFYPSAPFOEH-----LNFIAPETTG 170
Db      626 GGIYCGDDVTILNLGKTLFQENSEKRGGSLASLAKSKLTMWSLBSFCINATAENG 685

Qy      171 GCTRIPSFMSATHCYTHNVILSGCRDSSH-----QYALGVLTATATGRIF 220
Db      686 G-ANVP-----ENIVLPTPTPNEBAPVQPVYGBALVTGNTATKSGGIY 732

Qy      221 -----FSTLRSLSDDTONRKSCSVSATPLCCDMLCSKVTETEEDVNSAVPLIMAHGR 275
Db      733 TKNAAPSNLSSTYFPQNTSENGGALLTQKADATDCSFYITVNWLTNNATANGNGGIA 792

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276 GFDGQYHEKDLDTTLFEDWVANYPGVGSSFLDGRWFS--VYGLKPNSPDPTGOK 333
Db 793 G--GKAHFDRIIDLTV-----OSNOAKKGAGVLEDALEKVTIGSVSON---TATESG 842
Qy 334 VYIKRYNDTPDDEDDYQIRMAKSSYKPRGGRIOQALISIVYSTLGEDPVL---T 389
Db 843 GGIYAK-----DIQLOAL-----PGSF-----TTIDNKVETSLLTSTNLVGGGI 881
Qy 390 VPPVTVTLMAEG-----RIITVGTSHFLYORSSYFSPALLPYMTVSNKKTATLHSPY 442
Db 882 YSSGAVTLTNISGTFGTIGNSVINTATISODADIGGGIYA-----TTSLSINOCNTP 934
Qy 443 TF--NAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFYRNH-----GTMDSQARL 482
Db 935 LFSNNSAATKKTSTTKQIAGGAIPSAAVTIENNSQPIIFLNNSAKSEATTAATGNKOSC 994
Qy 483 -----TLRGVF-----GTMDSQARL 499
Db 995 GGAIAANSVTLTNPEITFKGNVAETGAIGCIDLTNGSPPRKVSADNGSVLFQDMSAL 1054
Qy 500 NPASAVPDSST--SRSRITRVSSSTK--AAVTTSTCF-----KVYKTKNTY 541
Db 1055 NRGAIYGETIDIRGTATPTFGNSKHDGSAICCTALTAPNSQLFENNKVETETATT 1114
Qy 542 CLSIAEISNTLFGFERRIVPLVEILKNDG 570
Db 1115 KASINNLGAAYGNNETSDVITISLAENG 1143

RESULT 4
US-09-841-132-394
Sequence 394, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatic, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841.132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 394
LENGTH: 1723
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-841-132-394

Query Match 4.8%; Score 144; DB 9; Length 1723;
Best Local Similarity 18.8%; Pred. No. 0.00035;
Matches 141; Conservative 88; Mismatches 284; Indels 236; Gaps 29;
Qy 4 AVSOVALEN--DEREAKNTWR-----LIFRAIILLTVTLATSVASIVSMG 49
Db 449 AVGOVTLIEDIANLKMNTNCKGEGAIYTKKALTINNAILTTSGNSTNGCAIFAVG 508
Qy 50 ASTPSDLVGT--PTRISRAEKITSALGNSODVYDRIYKOVALESPI-----94
Db 509 GITLSDIVEVRFSSKKTGNYGAPITKASNTAPVVS--SSTTASPAVPAAPAAAPVNA 565
Qy 95 -----ALNTEFTTINMAITSLOYINGAANNNGMGPFI-----HPPDI-----133
Db 566 AKGALVSTBELTVSGITSLISFENNECONOGGAYVTKTFOCSDSHLOFTSNKADEG 625
Qy 134 GGI--GKELIVDNASDVTSPYSAFOEH-----LNFIPAPTTGS 170
Db 626 GGLVCGDGVTLTNLTKTLFOENSEKKGGLSLASGSLMTSLESFCLANANTAKENG 685
Qy 171 GCTRIPSDMSATHCYHNANVILSGCRDHS--OYALGVLTATTATGRIF 220
Db 686 G-ANVP-----ENIVLFTYPTPTNEPAPVQPVYGEALVTGNATATYSGGCIY 732

221 -----FSTLSISIDPTONRKSCSVSATPLGCDMLCSKVTETEEDYNSAVPTLMAHRL 275
Db 733 TKNAFENLSVTFDQNTSSENGALLTQKRAADTDGSEFTYITVNTNNTATNGGGIA 792
Qy 276 GFDGQYHEKDLDTTLFEDWVANYPGVGSSFLDGRWFS--VYGLKPNSPDPTGOK 333
Db 793 G--GKAHFDRIIDLTV-----OSNOAKKGAGVLEDALEKVTIGSVSON---TATESG 842
Qy 334 VYIKRYNDTPDDEDDYQIRMAKSSYKPRGGRIOQALISIVYSTLGEDPVL---T 389
Db 843 GGIYAK-----DIQLOAL-----PGSF-----TTIDNKVETSLLTSTNLVGGGI 881
Qy 390 VPPVTVTLMAEG-----RIITVGTSHFLYORSSYFSPALLPYMTVSNKKTATLHSPY 442
Db 882 YSSGAVTLTNISGTFGTIGNSVINTATISODADIGGGIYA-----TTSLSINOCNTP 934
Qy 443 TF--NAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFYRNH-----GTMDSQARL 482
Db 935 LFSNNSAATKKTSTTKQIAGGAIPSAAVTIENNSQPIIFLNNSAKSEATTAATGNKOSC 994
Qy 483 -----TLRGVF-----GTMDSQARL 499
Db 995 GGAIAANSVTLTNPEITFKGNVAETGAIGCIDLTNGSPPRKVSADNGSVLFQDMSAL 1054
Qy 500 NPASAVPDSST--SRSRITRVSSSTK--AAVTTSTCF-----KVYKTKNTY 541
Db 1055 NRGAIYGETIDIRGTATPTFGNSKHDGSAICCTALTAPNSQLFENNKVETETATT 1114
Qy 542 CLSIAEISNTLFGFERRIVPLVEILKNDG 570
Db 1115 KASINNLGAAYGNNETSDVITISLAENG 1143

RESULT 5
US-09-975-719-405
Sequence 405, Application US/09975719
Publication No. US20030022349A1
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Rahme, Laurence G.
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361003
CURRENT APPLICATION NUMBER: US/09/975.719
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/199,637
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: US 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 405
LENGTH: 1198
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-975-719-405
Query Match 4.0%; Score 119; DB 11; Length 1198;
Best Local Similarity 21.3%; Pred. No. 0.06;
Matches 83; Conservative 53; Mismatches 112; Indels 142; Gaps 21;
Qy 59 IPT-----RIRAREKITSALGNSQDVV--DRIYQVAL--ESPALNTEFTTIN 105
Db 33 IPTWQORMTHQITRAKSLIAA--GCTLSTILFASDSYAATLANVSQOPFLV--TQVAPN 89
Qy 106 AITSL-----SYONGAANNNG-----WCAPLHDPDFIGIGKELIVDNASDVT 150
Db 90 LILFTLDSGSMAMAYVVDGISGNSGRAGRSSDVYALVYNDYAYOVKKTLLTSDQIIVS 149
Qy 151 FYP-----SAFOEHL-----NFIAPPTG-----SGC-----TRIP 176
Db 150 DYPVPRFAAMQDQVAGSTTNLSNNYRPMQGTGMLCIDSICNTGRAYVYTVKVSASC 209

177 SPDMATHYCYTHNVI--LSGRDHSCHOYLALGLVLT--TATGRIFPSTLRSLDTON 234
210 AQVYSSNSCYTNALPTSQESNPAIWTYRRRIATKTAALAPISLPENRL--TWGA 268
235 RKSCSVATPLGCDMLCSKYETEEDBDYNSAVPTLMAHGLGFGQYHEKDLDTTLFED 294
269 LNTCSIGANSRSCQ-----NNAL-----LQFNKQHKIN-----FFN 299
295 WYANVPVGG-----GSFIDRWVFSYVGLKXNSPSPVQEGK--YVYKXY--- 340
300 WLANSFASGGTPLHALDRAGRF-----LQNGTAAVTTEDEKTYSCRAASHYM 347
341 -----NDTCPEBODYQ 351
348 MTDGIMNGRNVTPGNLNDNGOTFPDSTLYR 377

RESULT 6
US-10-172-502-4
Sequence 4, Application US/10172502
Publication No. US20030165833A1
GENERAL INFORMATION:
APPLICANT: FOSTER, Timothy et al.
TITLE OF INVENTION: CROSS-REACTIVE MONOCLONAL AND POLYCLONAL ANTIBODIES.
FILE REFERENCE: P07263US01/BAS
CURRENT APPLICATION NUMBER: US/10/172,502
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/298,098
PRIOR FILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2283
TYPE: PRF
ORGANISM: Staphylococcus epidermidis
US-10-172-502-4

Query Match 3.9%; Score 116; DB 12; Length 2283;
Best Local Similarity 18.9%; Pred. No. 0.34; Indels 192; Gaps 25;
Matches 118; Conservative 82; Mismatches 231;

33 TVVTATLTSVAS--LVYMGASTPSDLVGIPTRISAREKITSALGNO-----DVID- 82
618 TVTWTVTGLPSGLSYD---SATNSIIIGTPKIGSVTVVSTDOANKKSTTTFTINVDT 674
83 -----RIYQVLALESPLAL--NTEITMAITSLSYQIN--GAANSGMGA 125
675 TAPVTPTDGOSSSEVSPV---SPIKATADNSGNAVTNTVTGLPSGLTPTDSTNTISGT 731
126 PIHPDPFIGIGKELELYDNASDVTSFVPSAFOEHLNFIAPATTGSGCTRIAPSPMSATHY 185
732 PTN-----IGSTI-----SIYS-----TDSAGKTTTTFYEVETRN 763
186 CYTHNVILSGCRDHS--HOYIALGVLTATTAIRIFSTLRSISLDTQNRKC 238
764 SMSQSVSTSGTQSGSVSTSKASQAS-----TSTSGIIVSTASST-----KST 811
239 SVSATPLGCDMLCSKYETEEDBD--YNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVA 297
812 SVS---LSDSVASAKSLSTSESNVSSSTSTSLVNSQSVSSM--SDSASKSTSLSDSIS 866
298 N-----YPGVGGSPFDGRVWFS 315
867 NSSSTKESSELSTSTSLRTSTSLSDLSLMSSTSGSLSKOSLSTISGSSSTASLSDS 926
316 VYGGILKEN-----SPSDTVQEGKVIYKRYNDTC--PDEODYOIRMAKSSYK----- 360
927 TSNAISSTLSSESASTSDSISINSIANSGASSTSDSGSTISLSTSDSKMSMTSES 966
361 -----PGRFGKRIQOAILISIVSTS-----LQEDPVLYTPENTVTLMGAEGLLT 406
987 LSDSTSTSGSVGSLIAASQSVSTSTSDSMSTSEIVSDSIST-----SGSLASDSKMS 1042

407 VCTSHFLYORGSYSPALYPMVTSNKTATLHSPYTNAPTRPGSIDCOASARCPNSCV 466
1043 VASSMSTSGSGST--SESLSDSGSTSDSDSKSLSGSTQSGSTSTSTSTASAVRSESGS 1100
467 TGVYTDPPPLPIFRNHTLRGVFTMLDSEQARLNPAASAFDSTSR-----ITRV 517
1101 TS-----GSMASQSDMSISTSPDSTSDSKASSTASSEISQS 1140
518 SSSSTKAATSTCFKVKYKNTK 540
1141 ASTSTSGSVSTISLSTNSERT 1163

RESULT 7
US-10-142-515-11
Sequence 11, Application US/10142515
Publication No. US20030078399A1
GENERAL INFORMATION:
APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
APPLICANT: Lloyd, Kenneth O.
APPLICANT: Yin, Beatrice W.T.
TITLE OF INVENTION: Nucleic Acid Sequence Encoding Ovarian Antigen, CA125, and Uses Thereof
FILE REFERENCE: 649-A-US
CURRENT APPLICATION NUMBER: US/10/142,515
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/290,480
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 5877
TYPE: PRF
ORGANISM: Human Being
FEATURE: MISC FEATURE
NAME/KEY: (1) (5877)
LOCATION: (1) (5877)
OTHER INFORMATION: Amino acid sequence of MUC16B
US-10-142-515-11

Query Match 3.8%; Score 114; DB 15; Length 5877;
Best Local Similarity 19.7%; Pred. No. 2.6; Indels 242; Gaps 35;
Matches 141; Conservative 96; Mismatches 236;

28 AILTLVTATLTSVASLVSMG-----ASTP--SDLVGIPTRISAREKITSAL--GSN 77
859 SVIADSVTKATISSMGIPTPTGDTNVLSTPAFSDSRIGT---KSKSLTGLMETSTIS 915
78 QDVDRIRYQVLALESPLALNTEITMAITSLSYQINCAANSGMGADIPDPFIGIG 137
916 EETSSATEKSTVLSSVPTGATTEVSRTAISSSRTSIPGAST-----MS 961
138 KEILVNASDVTSFVPSAFOEHLNFIAPATTG--SGCTRIAPSDM-----SATH 104
962 SDTSMETTRIST--PLTRKESTDMAITPKTGPAGATSGCTFLDSSSTASMPGTHSAT 1019
185 YCYTHNVILS-----GCRDS-----HSHQYIALGVLTATTAAG----- 217
1020 QRPFRSVVTPMSRGPEDVSWSPPLSVKNSPPSLVSSSVTSBPPLXSTSGSHSP 1079
218 ---RIFFSTLSIS--LDTQNRKSCSVSATPLGCD--MLCSKYETEEDBDYNSAVPTL 269
1080 VPYTSLFTSIMKATMDLASLEPETTSAPNNMITSDESLASKAT--TEETAIHVEENTA 1138
270 MAHGRIGFGQHEKDLDTTLFEDWVANYPG-----YGGGSPFDGRVWFSYV 318
1139 ASH-----VETTSATEELYSPPGSEPTKVISPVTSSSIRDNVNSTTTPG 1185
319 -----GLKPNSPDV---QEGKVIYKRYNDTCPPDQDYOIRMAKSS 358
1186 SSGITTEIESMSSLTPGLRETRTSODITSTSTSTVILKMGSGATPEVSRREVMSKRT 1245
359 YKPRFGKRIQOAILISIKVS-----TSLQEDPVLT-----TVPN 393

Db 1246 SIFGP-----AOSTMSLIDSEVYTRLSTSEIMESAEITTTTGTGSLATSOVTLPLG 1299
Qy 394 T-VTMAGBGRILTVGTSHF-----LYORGS---SYFSPALL-----YPMW---VS 432
Db 1300 TSMFTLDSGTHSMGGLSHSEMTLMMSRGPESLSTSPFVETTRSSSLSLTLTSLS 1359
Qy 433 NKTATL-----HSPYTFNAFTPRG-----SIFCOASARCPNSCVTGVYTDVPL 476
Db 1360 FVSSTLDSPPSPPLPVTSLLPLGLVKTEVLDTSSEPKTSSS---PNLSSTSV----- 1410
Qy 477 IFYRNHTLRGVFTMLDSEQ-----ARLNPAASAVFDS-----TSRRTIRVSSSS 521
Db 1411 -----EIPATSEIMTDEKHPSSNTAVAKVRTSSVHSHSVLADSEITTTTIPSMGI 1464
Qy 522 TKA-----AYTSTGCF---KVKTKNTKYCL-----SIAEISNTLFG 554
Db 1465 TSAVEDTTVFTSNAPFSETRRIPIETPFSLTPGPRETSTSEETTSITETSAVLFG 1519

RESULT 8
US-10-243-243A-8

Sequence 8, Application US/10243243A
Publication No. US2003010442A1
GENERAL INFORMATION:
APPLICANT: Lleyd, Kenneth O.
APPLICANT: Yin, Beatrice W.T.
TITLE OF INVENTION: Nucleic Acid Sequence Encoding Ovarian Antigen, CA125, and Uses T
FILE REFERENCE: 649-B
CURRENT APPLICATION NUMBER: US/10/243,243A
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 10/142,515
PRIOR FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: PCT/US02/14766
PRIOR FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: US 60/290,480
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 5935
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1) (5935)
OTHER INFORMATION: Amino acid sequence of MUC16B
US-10-243-243A-8

Query Match 3.8%; Score 114; DB 15; Length 5935;
Best Local Similarity 19.7%; Pred. No. 2.6;

Matches 141; Conservative 96; Mismatches 236; Indels 242; Gaps 35;

Qy 28 ALLTLTVTLATSVASLVYSMG-----ASTP---SDLVGIPTRISPAEKITSAL---GSN 77
Db 930 SVLADSVTTKATSSMGITYPGDTNVLSTPAFSDTSIQT---KSLSLPGLMETSLIS 986
Qy 78 QDVVDRIKQVABEPLALNTETITMAITSLSQINGAANSCWGAIPHDPDTGIG 137
Db 987 EETSSATEKSTVLSVPTGATTEVSRTRAISSRSISIGPPOST-----MS 1032
Qy 138 KELIYDNASDVTSFPFSAFOEHLNFIAPPTG---SGCTRIPSFDM-----SATH 184
Db 1033 SDTSMETTRIST---PLRKSESTDAITPKTGPSGATSGGFTTLSSSTASMPGTHSAT 1090
Qy 185 YCYTHNVLS---GCRDHS-----HSHOYLALGVLRITATG----- 217
Db 1091 QRFPRSVVTTTPMSRGPEDEVSWPSPLSVEKNSPSPSSVSSVTSPLXSTPSSGSHSP 1150
Qy 218 -----RIFSTLARSIS---LDDTONRKSQSVSATPLGCD---MLCSKYTEEBEDYNNAVPTL 269
Db 1151 VPTVSLSTLSIMKATMDLADSLSEPTTSAPNMNITSDSLASKAT-TETEAHVFEENTA 1209

Qy 270 MAHGRIGFGQYHEKDLDTVTLTFEDVWVANYPG-----VGGGSFLIDGRVWFVYG 318
Db 1210 ASH-----VETTSATELELVSSSPGFSEPTKVISPVVTSSIRNNWSTTMPG 1256
Qy 319 -----GLKNSPQDV---QBEKVYIYKRYNDTCDEBDYQIRMAKS 358
Db 1357 SSGITRRIEBSMSLTPGLRETRISODITSTSTETSVLYKMPGATPEVSRTEVWPSRT 1316
Qy 359 YKPRFGGKRIQQAILSIRKS-----TSIGEDPVV-----TVPN 393
Db 1317 SIFGP-----AOSTMSLIDSEVYTRLSTSEIMESAEITTTTGTGSLATSOVTLPLG 1370
Qy 394 T-VTMAGBGRILTVGTSHF-----LYORGS---SYFSPALL-----YPMW---VS 432
Db 1371 TSMFTLDSGTHSMGGLSHSEMTLMMSRGPESLSTSPFVETTRSSSLSLTLTSLS 1430
Qy 433 NKTATL-----HSPYTFNAFTPRG-----SIFCOASARCPNSCVTGVYTDVPL 476
Db 1431 FVSSTLDSPPSPPLPVTSLLPLGLVKTEVLDTSSEPKTSSS---PNLSSTSV----- 1481
Qy 477 IFYRNHTLRGVFTMLDSEQ-----ARLNPAASAVFDS-----TSRRTIRVSSSS 521
Db 1482 -----EIPATSEIMTDEKHPSSNTAVAKVRTSSVHSHSVLADSEITTTTIPSMGI 1535
Qy 522 TKA-----AYTSTGCF---KVKTKNTKYCL-----SIAEISNTLFG 554
Db 1536 TSAVEDTTVFTSNAPFSETRRIPIETPFSLTPGPRETSTSEETTSITETSAVLFG 1590

RESULT 9
US-09-815-242-12713

Sequence 12713, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zykend, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA-011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12713
LENGTH: 2344
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12713

Query Match 3.8%; Score 112.5; DB 9; Length 2344;
Best Local Similarity 18.9%; Pred. No. 0.8;
Matches 125; Conservative 89; Mismatches 251; Indels 195; Gaps 24;

QY 33 TTVTLATSVAS-LVYSMGASPPDLVGIPRTISPAEEKITSLASNQ-----DVIDR 83
Db 606 TVTNTVIGLPGSLGYD---SATNSIIIGFPIKIGSGTYVTVSTDDANKSTTTFTINAVDT 662
QY 84 IY-----KQVALESPPLALLNTEY-----TMMATISLSYOIN-GAANNSGMAPIH 128
Db 663 TAPVTVEIDGSSVFPSPISPINATQDNGNAVNTVGTGPGSLTFPDSITNNTISGTPTN 722
QY 129 DPDIIGIGIKELIYDNASDVTSFYPFAFQEHNLNIPAPTTSGCGCTRIISPFMASITHCYT 188
Db 723 -----IGSTITTVSTD-----ASGNKTTTTFEYEVTRNSMS 754
QY 189 HNVILSGCRDHS-----HOYLALGVLTATTATGRIFFSTLISLSDYQNRKSGSVS 241
Db 755 DSVSTSGSTQSGSVSTSKADSQAS-----TSISGSIIMSTSASTS-----KSTNSV 802
QY 242 ATPLGCMCLCSKVTETEBED-YNSAVPTLMAHGRIGFDGYCHEKDLVYTLIFEDMVAN-- 298
Db 803 ---LSDSVSASKSLSTESBNSVSSSTSTSLVNSOSVSSSM--SGSVSKSTSLDPFISNS 857
QY 299 -----YPOVGGGSPIDGRVMPFVYGGKLPN-----SPSDTVQEBKVIYIKRYN 341
Db 858 STEKSESVSTSTSLRSTSLSDSVMSMTSGSLSKSGSLSTSTSDASMTSGSVSDSTSN 917
QY 342 DTCPEQ-----DYQIRAKSSYKPGFSGKRIQQAIIISKVTS-----381
Db 918 SITSSESLSESGSTSEGISINSISNSVSASTSKLESQSTISLSTSDSKMSSTESISLD 977
QY 382 -----LGEDPVLTVPNTV-----TLMGABGRILTYGTSHFL 413
Db 978 STSTSDSVSGSLSVAGSQSVSTSTSDSMSTSEMISDSMTSGSLAASDKMSVSSSNST 1037
QY 414 YORGSYFSPALLYPMTVSNKATILHSPYTFPNAFTRPSPGIPCOASARCPNCGVYVTPD 473
Db 1038 SQSGST--SESLDSISITSDSDSKSLSTSQSGSTISITSTSSVMSSEQSTS----- 1090
QY 474 YPLIFRNHTLRGVFGTMLDSEQARLNPAASAVPSTSR-----ITRVSSSTKA 524
Db 1091 -----GSMSTSQSDSTSTSTSFSDSTSTSKASVASESISIQSVSTSTSG 1135
QY 525 AYTSTCFKVKTKTKT-----YCLSLAEISNLTFGFRVPLVLLVELKNDGVRERASG 577
Db 1136 SVSTSTSLSTNSBERTSTMSDSTSLSTSESDST-----SDSTSTSDSISEAISG 1185
RESULT 10
US-09-965-738-146
Sequence 146, Application US/09965738
Publication No. US20030143667A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy
TITLE OF INVENTION: Repeat Sequences of the CA125 Gene and Their Use for Diagnostic a
FILE REFERENCE: 40715-258841
CURRENT APPLICATION NUMBER: US/09/965,738
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/284,175
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 306
SOFTWARE: PatentIn version 3.0
SEQ ID NO 146
LENGTH: 9799
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1) --(9799)
OTHER INFORMATION: Any "X" = any amino acid
US-09-965-738-146

[illegible]

Query Match	3.7%	Score 11;	DB 12;	length 9799;
Best Local Similarity	19.8%	Pred. No. 12;		
Matches 117;	Conservative 76;	Mismatches 198;	Indels 200;	Gaps 28;

Query Match	Score	DB	Length
3.7%	111	12	11721

Matches 117; Conservative 76; Mismatches 198; Indels 200; Gaps 28;

31 LTTVTLATSASLVSMGASTPSDLVGIPTRISRAEKITSA LGS--NQDVDRIRYKQ 87

DB 2892 LVPFTLNFTTNLOYEEDMRPG-----SRKNATERVLOGLSLPFKNSSVGPPLYSG 2945
QY 88 VALSEPLALLNTETTINMAITSLSYOINGAANNNGWAPIHDPDFIGIGKELIYDNASD 147
DB 2946 CRL-----TSLREKDGAAATGMADVCLYHNPNRKGPDRLRQULWELSQ 2988
QY 148 VT-----SFYPSAFQEHANFIPA-----PTTGS-----GC 172
DB 2989 LTHNITELGPYSLDRDSLIVNGF--THONSVPPTTSPPGSTVYMAWATTGPPSSPFGHTBGP 3047
QY 173 TRIP-SFPMASATHYCYTNHVLISGCRDHSHQVALAVL-----RTTANRFFESTLASI 227
DB 3048 LIIPFTFNFTTNLHAYEENMOHPSGRKNTTERTVLQ--GLKPLFKNTSVGPL--YSGCRLT 3105
QY 228 SLDDTQ-----NRKSCSVATPLGDM--LCSKYTEEEDYNSAFTLM 270
DB 3106 SLRPEKDGAAATGMADVCLYHNPNRKGPDRLRQULWELSQ-----PSTL 3157
QY 271 AHGRLGPDQYHEKDLVTTLFEDWVANYPGVGGSPIDGRVWFSVYGGLKPNSPSDTVQ 330
DB 3158 DRDSLIVNGFTHONSVPPTTS-----PCT-----STVYMAWTTG--FPSSPFGHTE 3200
QY 331 EGVYIYKRYNDTCDEBODYQIRMAKSSYKPG--RFG--GKRIQOAILG--IKVSTSLGE-- 384
DB 3201 PGLIIPFTFNFTTN-----LHAYEENMOHPSGRKNTTERTVLQGLKPLFKNTSVGPLY 3255
QY 385 -----DPV-----LTVPNTVTLMAGBRIL 405
DB 3286 SGCRLTLRPEKHEATGVDTICTHRVDPISGDLRRELYWELSQLTMSITELGP----- 3310
QY 406 TVGTSHPLYORGSY--FSPALLYPMVSNKTATLHSPYTFNAFTRPGSIPCOASARCP 462
DB 3311 -----YTLDRDSLIVNGFNPRSSVPTTSTPGTSTVHLATSGTSPSLPG----- 3353
QY 463 NSCVTVGVTDPVPL--FYRNHTLGVFGCTMLDSQALNPAVFDSTSR 511
DB 3354 -----HTAPVPLIIPFTLNFTTN-----TNLHAYEENMOHPSGRKNTTERT 3392

RESULT 12

US-09-738-626-3707
; Sequence 3707, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3707
; LENGTH: 1510
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3707

Query Match 3.7%; Score 109.5; DB 10; Length 1510;

Best Local Similarity 20.1%; Pred. No. 0.77;
Matches 99; Conservative 63; Mismatches 181; Indels 149; Gaps 24;
QY 47 SMGASTPSDL-----VGIPTRISRAEKITSLGNSODPV-----DHRYKVALESPLAL 96
DB 576 SFGAAVLSGLYPAVHAGKMAIAIARVREVESEAIRKGTILYVSDSEDERMAPIPALL 635
QY 97 L-----NTETTINMAITS--LSYOINGAANNNGWAPIHDPDFI-----G 134
DB 636 LTSAVHGYLVQQRRTQCSLVESGDAREVHMLLIGFADAINPVAPEITDELNRKG 695
QY 135 GIGKELIYDNAS-----DVTSTFSPAFQEHINF 162
DB 696 QLG-DLSIDEASRYIKAATTGVLKWSKGIATVSSYRGQQLADVGLHQDLIDNYFGG 754
QY 163 IPAPTTSGCRRISFPMASATHYCYTNHVLISGCRDHSHQVALG----- 209
DB 755 IASPISGIGLDEVAA--DVEARH--RSAPLP--RPEHAREIDLGGYKMRREGEVHL 807
QY 210 -----VLTATATG--RIFFSTLRISLDDTQNRKSCSVATPLGDMLCSKYTEEE 259
DB 808 FNPETIRKQAHATSSGSEYEIFKDYTRKY--DDOSTRLGTIRGLFEPSTDRKPIVSSEVP 865
QY 260 EDYNSAVPTLMAHGRIGPDQYHEKDLVTTLFEDWVANYPGVGGSPIDGRVWFSVYGG 319
DB 866 V---SEIVKRFSTGAMSY--GSIASAEHEVLIANNRILGMSNSGEGG--EDARRF-----D 915
QY 320 LKEN-----SPSDYVQSGKYIYKRYNDTCDEBODYQIRMAKSSYKRGFKRIQOAIL 374
DB 916 VEPNGDMKRSIAIKOVASGRFQVTSYHLNCC--TDIOIKAAQGA--KQGE--GGQ----- 963
QY 375 SIKVSTSLGSDPVLTVPNTVTLMAGBRILTVGTS-----HFLYORGSYSPALLY 427
DB 964 -----LFPNKYVWVAEVRITTBVGSLSPRHDIY-----SIDLAQLIH 1005
QY 428 PMTVSNKTATLH 439
DB 1006 DLKANPRAIRH 1017

RESULT 13

US-10-369-493-1535
; Sequence 1535, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369, 493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360, 039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1535
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1535

Query Match 3.6%; Score 108; DB 12; Length 1609;
Best Local Similarity 19.4%; Pred. No. 1.2;
Matches 123; Conservative 79; Mismatches 227; Indels 206; Gaps 23;

QY 30 LLLTVVTLATSVASLVSMGASTPSDLVGIPTRISRAEKITSLGNSODVBRIRYQV-- 88
DB 748 LVLSVTVTYVNGAATETTCWC--PASSIAVTTTSSITVTLVLTVEVCSHSGCTPTVITSVT 805
QY 89 ALSEPLALLNTETTINMAITSLSYOINGAANNNGWAPIHDPDFIGIGKELIYDNASDV 148

Db 806 ATSTTIPLLSTSSS-----TVLSTVEGAKN----- 832
Qy 149 TSPYPSAPQEHLPNIPAPVTGSGCTRIAPSPDMKATHCYTHNVILSGCRDHSHOYIAL 208
Db 833 -----PAASEVTINTQVATSEARST-----STQVSAATATAAASSTTSQVSTASETISTL 885
Qy 209 GVLRTTATGRIFPFTLSISLDDT-ONRKSQVSATPLGDMLCNKVTEEDDYNSAVP 267
Db 886 GTQNFPTTGSLLPPLALSTEMINTTVSRKLIIS-----TEVSHSKCVP 930
Qy 268 TLMAN-GRLGFDGQYHEKD-----LDVTTLFEDWVANYPGVGGGFLDGRVWFSV-- 316
Db 931 TVITEVNTSGTSPNGSHSQTLQTEAVEVTLSSHQVTVMTSEVCSNICTPVTITSQVR 990
Qy 317 ----YGLKPNSPSPVTVEGRVVIKRYND-----TCDEDDYQIRMAKSS 358
Db 991 STPEPYLTSTSSSLASTKSSLSLASESEMTSPVSTQSLPLFTCSEK-----RST 1042
Qy 359 YKGRFGGRKIQQAILSIKYST-SLGEDPVLTPPNTVTLMGAGRILTVGSHFLYQRG 417
Db 1043 TSVSQMNTVLTNTIMSSSNVISTNKPSTTSP-----YNFS 1081
Qy 418 SSYFSPALLYPMTVSNKTAT-----LHSPYT-----FNAFTR 449
Db 1082 SGYSLPSSSTPSQYSLSTATTTTNGIKTVYTWCPLEKSTVAASSQSRSVDRFVSSSK 1141
Qy 450 PGSLPCQASARCPNSCT-----GYTDPYPLIFRNTLKGVCFTMDSEQARLNP 502
Db 1142 PSSSLSGTSTIQYTLSTATTITISGLKTYVTTWCP-----TSKSTLG-----A 1183
Qy 503 SAVDSTSRSRITRVS-SSTKAAVTTST-----CFKVVTKNTK-- 540
Db 1184 TTQTSSTAKYRITSASSATSTISLSTSTSESSSGYLSKGVCSGCTCTQDVPTQSSSPA 1243
Qy 541 ----YCLISIAEIS-----NTLFGFRIIVPL 562
Db 1244 STLAYSPPSVSTSSSSFSSTTASTLTSTHTSVPL 1278

RESULT 14
US-10-032-189-128
Sequence 128, Application US/10032189
Publication No.: US20030170630A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zehrhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Groves, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Shinkets, Richard A
APPLICANT: Groves, William M
APPLICANT: Szekeres, Edward S
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc L
APPLICANT: Gorman, Linda
APPLICANT: Gangoli, Neha A
APPLICANT: Fernandes, Elma R
APPLICANT: Rieger, Daniel K
APPLICANT: Edinger, Shlomit R
APPLICANT: Gunther, Erik
APPLICANT: Miller, Isabelle
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Macdougall, John R
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/282,981
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/309,247
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 128
LENGTH: 5636
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (3003)
OTHER INFORMATION: wherein Xaa is any amino acid.
FEATURE:
NAME/KEY: VARIANT
LOCATION: (3041)
OTHER INFORMATION: wherein Xaa is any amino acid.
FEATURE:
NAME/KEY: VARIANT
LOCATION: (3367)
OTHER INFORMATION: wherein Xaa is any amino acid.
US-10-032-189-128

Query Match 3.6%; Score 108; DB 12; Length 5636;
Best Local Similarity 21.8%; Pred. No. 9.5; Indels 184; Gaps 35;
Matches 131; Conservative 65; Mismatches 221;
Qy 20 TWRLPRIALILLTVYVLTATSVASLVYSGASTPSDVGIPTRISRAE--KITSALGSN 77
Db 3 SWEVHTVFLFALLVSSLA-----ODASPOSEI-----RAEFPPGASTLAV 45
Qy 78 ODVVDRIYKQV--ALESPLALNTETTTNNATTSLSYQINGAANSGWGAPIHDPDFIG 135
Db 46 PDVTGSMYDDLVQVIEGASKIL--ETSLKRPKRPV--FNPL-----VPRHDE-- 90
Qy 136 ICKELIVNASDVTSTYPSAPQEHLPNFT-----PAPTGSCTRIIP-----SF-- 178
Db 91 IGPVITITD-----PKKFQYELRELYVGGGDCPEMSIAIKALEISLPGSFYVF 142
Qy 179 -DMSATHYCYTHNV-----ILSG-CRDHSHOYIALGVLTATNGRIFF-- 221
Db 143 TDARSKDYLTHREVLOLIQKQSQVVFVLTGDCDDRTI--GKYVTEIATSTSGQVFHLD 201
Qy 222 -----STLRSISLDDTONRKSQVSATPLGDMLCNKVTEEDDYNS 264
Db 202 KKQVNEVLKWEAVQASKVHLSTDHLEQ--AVNTWRIPFDSLKEVT-----VSL 251
Qy 265 AVPTLMAN-----GRL-----GFDGQYHE-----KDDVTTLFED-----WYANPGV-- 303
Db 252 SGSPMIEIRNPLGKLIKKGFG--LHELLINHSKAVNVKPEAGMTVTKSSGGRHSV 309

QY 304 ----GGSFIDGRWSEVYGLKP-----NSPSDTVOE-GKVIYIKRYNDTCPEBODY--OI 352
 Db 310 RTTGSTIDFRAGFS-----RKPTLDFKTVSRPVGIPYIVLINTSGISTPARIDLEL 365
 QY 353 RMAKSSYK--PGRFGKRIQQAIIISIKVSTSLGEDVULVPPNVTIIMGABEGRILTGTGS 410
 Db 366 SISGSSLKTIPIVKYIHRKPYGIWNISD-----FVPPNEAFELKVTG---YDKD 411
 QY 411 HFLYORGSSYFSPALLYP---MTVSNKTATLHSPYFNATFRPGSIPCOASARCPNSCV 466
 Db 412 DYLFQRYVSS-VSFSSIVDPAPKVTMEKTP-----GYILOPQOIFCSVDLSL----- 457
 QY 467 TGVYTDYPIIFYRNHTLRCVFGTMDSEQARLNPASAVFDSTSRITRVSSSSSTKAY 526
 Db 458 -----PFTLSFVRNGVTLGVDOYLKESASVSLIDIAKVTLSDEGFYECIAVSSAGTGRAQ 511
 QY 527 T 527
 Db 512 T 512

RESULT 15

US-10-120-801-72

Sequence 72, Application US/10120801

Publication No. US20030203843A1

GENERAL INFORMATION:

APPLICANT: Pena, Carol

APPLICANT: Guo, Xiaojia

APPLICANT: Shimkets, Richard

APPLICANT: Padigaru, Muralidhara

APPLICANT: Kerkuda, Ramesh

APPLICANT: Spytek, Kimberly

APPLICANT: Mehraban, Foad

APPLICANT: Topper, James N.

APPLICANT: Malyankar, Uriel

APPLICANT: Wasserman, Scott

APPLICANT: Edinger, Shlomit

APPLICANT: Smithson, Glennda

APPLICANT: Gunther, Erik

APPLICANT: Komuves, Laszlo

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-140

CURRENT APPLICATION NUMBER: US/10/120,801

PRIOR FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 60/285748

PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: 60/286068

PRIOR FILING DATE: 2001-04-24

PRIOR APPLICATION NUMBER: 60/286292

PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: 60/288334

PRIOR FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: 60/291241

PRIOR FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 60/322284

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: 60/285609

PRIOR FILING DATE: 2001-04-20

NUMBER OF SEQ ID NOS: 155

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 72

LENGTH: 5636

TYPE: PRY

ORGANISM: human

FEATURE:

NAME/KEY: VARIANT

LOCATION: (3003)

OTHER INFORMATION: wherein Xaa is any amino acid.

NAME/KEY: VARIANT

LOCATION: (3041)

OTHER INFORMATION: wherein Xaa is any amino acid.

NAME/KEY: VARIANT
 LOCATION: (3367)
 OTHER INFORMATION: wherein Xaa is any amino acid.
 US-10-120-801-72

Query Match 3.6%, Score 108; DB 12; Length 5636;
 Best Local Similarity 21.8%; Pred. No. 9.5;
 Matches 131; Conservative 65; Mismatches 221; Indels 184; Gaps 35.

QY 20 TWRLIFRAIILLVVTIATISVSLVSMGASTPSDLVGIPTIRISRAEE-KITSALGSN 77
 Db 3 SWEVHTVFLPALIYSSIA-----QDASPOSEI-----RAEEFEGASTIAFV 45
 QY 78 QDVVDRIKQV--ALESPALINTETITMAITSLSVQINGAANNMGCAIHPDPFIC 135
 Db 46 FVVGSMYDDLVQVIBGASKTL--ETSLKRPKRL--FNAL-----VFHDEP 90
 QY 136 IGKELIVDNASDVTSFYPSAFQEHNF-----PAPYSGGCTRIIP-----SF 178
 Db 91 IGVTLITD-----PKKQYELRELYVGGGDCPEMSGAIKIALEISLPGSFYVF 142
 QY 179 -DMSATHYCYTHN-----ILSG-CRDHSHQYALGVLRITATGRIFP-- 221
 Db 143 TDARSKDYRLTHEVLQIQKQSQVVFVLTGDCBDRTHI-GYKVEEIASTSGQVPHLD 201
 QY 222 -----STLSISLDDTONRKSGSVSATPLGCDMLCSKYTETEEDYNS 264
 Db 202 KKQVNEVLKAVEEAVQASKVHLSTDLHQ--AVNTWRIPEPUSLKEVT-----VSL 251
 QY 265 AVPTLMAN-----GRL--GFDQYHE-----KDLDTTLFED--MVANYPGVG-- 303
 Db 252 SGPSPMIEIRNPGLKIKGFG--LHLLNHNHSAKVNVKPEPAGMWYTKTSSGHSV 309
 QY 304 ----GGSFIDGRWSEVYGLKP-----NSPSDTVOE-GKVIYIKRYNDTCPEBODY--OI 352
 Db 310 RTTGSTIDFRAGFS-----RKPTLDFKTVSRPVGIPYIVLINTSGISTPARIDLEL 365
 QY 353 RMAKSSYK--PGRFGKRIQQAIIISIKVSTSLGEDVULVPPNVTIIMGABEGRILTGTGS 410
 Db 366 SISGSSLKTIPIVKYIHRKPYGIWNISD-----FVPPNEAFELKVTG---YDKD 411
 QY 411 HFLYORGSSYFSPALLYP---MTVSNKTATLHSPYFNATFRPGSIPCOASARCPNSCV 466
 Db 412 DYLFQRYVSS-VSFSSIVDPAPKVTMEKTP-----GYILOPQOIFCSVDLSL----- 457
 QY 467 TGVYTDYPIIFYRNHTLRCVFGTMDSEQARLNPASAVFDSTSRITRVSSSSSTKAY 526
 Db 458 -----PFTLSFVRNGVTLGVDOYLKESASVSLIDIAKVTLSDEGFYECIAVSSAGTGRAQ 511
 QY 527 T 527
 Db 512 T 512

Search completed: January 2, 2004, 16:25:03
 Job time : 54 secs

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